

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 1, 2002, 21:19:11 ; Search time 21 Seconds

(without alignments)
1803.665 Million cell updates/sec

Title: US-09-732-597-2

Perfect score: 2062
Sequence: 1 MALKLNFOCKKNHPAFAKS.....KKKAHPVPSFWMFNRELEKI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1545.5	75.0	385	2	A47245 acyl-[acyl-carrier
2	1490	72.3	396	1	OHCSAD acyl-[acyl-carrier
3	1422.5	69.0	411	2	T07806 acyl-[acyl-carrier
4	1410.5	68.4	399	1	OHSPAD acyl-[acyl-carrier
5	1408	68.3	396	2	B39170 acyl-[acyl-carrier
6	1406	68.2	396	1	A39173 acyl-[acyl-carrier
7	1396	67.7	398	2	S23351 acyl-[acyl-carrier
8	1395	67.7	396	2	T14264 acyl-[acyl-carrier
9	1386.5	67.2	393	2	S44202 acyl-[acyl-carrier
10	1386.5	67.2	399	2	S24995 acyl-[acyl-carrier
11	1385.5	67.0	393	2	T07633 acyl-[acyl-carrier
12	1381.5	67.0	401	2	ER4869 acyl-[acyl-ACP desat
13	1381	67.0	396	2	T14268 acyl-[acyl-carrier
14	1375.5	66.7	397	2	T10793 acyl-[acyl-carrier
15	1352	65.6	396	2	T14172 acyl-[acyl-carrier
16	1347.5	65.3	407	2	S71264 acyl-[acyl-carrier
17	1320.5	64.0	394	2	T51494 acyl-[acyl-carrier
18	1310.5	63.6	390	2	T04097 acyl-[acyl-carrier
19	1246	60.4	396	2	S31959 acyl-[acyl-carrier
20	1223.5	59.3	401	2	T51493 acyl-[acyl-carrier
21	1197	58.1	374	2	A96502 acyl-[acyl-carrier
22	295	14.3	328	2	T35035 probable acyl-[acyl
23	271.5	13.2	338	2	DB182 acyl-[ACP] desatur
24	256.5	12.4	338	2	H70810 probable desat pro
25	135	6.5	275	2	C87153 acyl-[ACP] desatur
26	122.5	5.9	2269	2	T28677 rhogly protein -
27	121.5	5.9	275	2	D70896 probable desat pro
28	114.5	5.6	1557	2	T18412 lipid-binding prote
29	108	5.2	616	2	A64341 hypothetical prote

30	105.5	5.1	393	2	C71836 tryptophan synthas
31	105.5	5.1	520	2	F90596 restriction-modifi
32	105.5	5.1	520	2	A99565 restriction-modifi
33	105.5	5.1	684	2	AE2004 hypothetical prote
34	104.5	5.1	524	2	T43050 cyclin E - Caenorh
35	104.5	5.1	570	2	T30156 hypothetical prote
36	103	5.0	244	2	C89811 hypothetical prote
37	102.5	5.0	393	2	F64679 tryptophan synthas
38	102.5	5.0	520	2	S49395 HsdM protein - My
39	101.5	4.9	846	2	JC7720 acetyltransferase
40	100.5	4.9	1027	2	T46296 hypothetical prote
41	100.5	4.9	3643	2	T36410 probable polypeptid
42	100	4.8	604	2	T19682 hypothetical prote
43	99.5	4.8	517	2	T48283 ankryn-1-like prote
44	99.5	4.8	1120	2	JC7765 mitotic spindle as
45	99	4.8	782	2	A82940 hypothetical prote

ALIGNMENTS

RESULT 1

A47245
N:Alternate names: type II acyl-ACP desaturase
C:Species: Coriandrum sativum (coriander)
C>Date: 21-Jan-1994 #sequence_rev18-Nov-1994 #text_change 03-Jun-2002
C:Accession: A47245
R:Cañon, E. B.; Shanklin, J.; Ohlrogge, J. B.
Proc. Natl. Acad. Sci. U.S.A. 89, 11184-11188, 1992
A:Title: Expression of a coriander desaturase results in petroselinic acid production
A:Reference number: A47245; M0ID:93087491; PMID:1454797
A:Accession: A47245
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-385 <CAH>
A:Cross-references: GB:M93115; NID:q167388; PIDN:AAC63059.1; PID:q167389
A>Note: sequence extracted from NCBI backbone (NCBIN:119750, NCBI:P.119751)
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase

Query Match	Best Local Similarity	75.0%;	Score 1545.5;	DB 2:	Length 385;
Matches	296;	Conservative	42;	Mismatches	36;
				Indels	31;
				Gaps	5
QY	1	MALKLN----	FOCKKNHPAFAKSP	PLPVRVSSP-----	RYFMASTVNSNMYLNLK 49
DB	1	MALKLNALMTLQCKRN-----	MTRTAPQAGRVSKVSMAS	TLHASPVPFKLK 51	
QY	50	SPPNLQVTHSMPOKLEIFKSLDDMARNNVLIHLKSVKSMOPD	YLPDPVSDFEQRV 109		
DB	52	AG-----	REVDELFLNLSGWARDN	LIHLKSVENSMQPDYLP	PDTSDFEQVK 102
QY	110	ELBRKEIIPDDYFVLVGMITEBALPTYMSMLNRC	DGKIDETGAPSSAMAMWTRAWTA 169		
DB	103	EMREKAKIIPDEFYVLVGMITEBALPTYMSMLNRC	DDIKDGTGAPTSWATTRAWTA 162		
QY	170	EENRHGDLNKYLYLSGRVDMRKIE	KTYOYLISGMSDKSENSPYLGFI	YTSFOERATFI 229	
DB	163	EENRHGDLNKYLYLSGRVDMRKIE	KTYOYLISGMSDFTENC	PLYMGFI	YTSFOERATFI 222
QY	230	SHANFTAKLAOHYGDKNLAHIGS	IASDEKRRHATYTKIVKLAETD	PDPTVIAFAADMRK 289	
DB	223	SHANFTAKLAOHYGDKNLAHIGS	IASDEKRRHATYTKIVKLAETD	PDPTVIAFSDMRK 282	
QY	290	KITMPAHLMTDGSDELFRKFT	PAVAVXYSALDYCDILEFL	VDKMNERLGLSDEGR 349	
DB	283	KITMPAHLMTDGSDELFRKFT	PAVAVXYSALDYCDILEFL	VDKMNERLGLSDEGR 342	
QY	350	KAOEYVCELGPKIRVEKEVQKKEKKKAHPVPS	WMFNRELEKI 394		
DB	343	KAOEYVCELGPKIRVEKEVQKKEKKKAHPVPS	WMFNRELEKI 385		

RESULT 2

OHC5AD

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - castor bean
 N:Alternate names: stearyl-[acyl-carrier-protein] desaturase
 C:Species: Ricinus communis (castor bean)
 C>Date: 31-Dec-1992 #sequence-revision 31-Dec-1992 #text-change 03-Jun-2002
 C/Accession: S16463; A39170

R:Knutzon, D.S.; Scherer, D.E.; Schreckengost, W.E.
 Plant Physiol. 96, 344-345, 1991
 A:Title: Nucleotide sequence of a complementary DNA clone encoding stearyl-acyl carrier
 A:Reference number: S16463
 A:Accession: S16463

A:Molecule type: mRNA
 A:Residues: 1-396 <KNV>
 A:Cross-references: EMBL:X56508; NID:g21092; PIDN:CAA39859.1; PID:g21093
 R:Shanklin, J.; Somerville, C.
 Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
 A:Title: Stearyl-acyl-carrier-protein desaturase from higher plants is structurally uni

A:Reference number: A39170; MUID:91172837; PMID:2006187
 A:Accession: A39170
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-396 <SHA>
 A:Cross-references: GB:M59858

A>Note: Parts of this sequence were confirmed by peptide sequencing
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase
 C:Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase
 F:1-33/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F:34-396/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match Best Local Similarity 72.3%; Score 1490; DB 1; Length 396;
 Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

OY 1 MALKLN-FQCKKNHFAFAKSPLEVTFRVSPRVMASTVNSNVLDNLKSP-----PN 53
 Db 1 MALKLNFLSQTOFKLPFALPMASTR--SPKFTMASTLSSGSEVENLKKPMPREHV 58
 OY 54 LQYTHSPPOKLEIFKSLDWMARNVLIHLKSVKSWQPODYLDPVSDGFEQVRELE 113
 Db 59 VQYTHSPPOKLEIFKSLDWMARNVLIHLKSVKSWQPODYLDPVSDGFEQVRELE 118
 OY 114 RAKEIPDDYFVVLVGMITEALPTYSMLNRCDGIDETGAEFSANAMTTRAVTAENR 173
 Db 119 RAKEIPDDYFVVLVGMITEALPTYSMLNRCDGIDETGAEFSANAMTTRAVTAENR 178
 OY 174 HGDLLNKYLYLSGRVDMRKTEKTIOYLIGSGMDIKSENSPYLGFTYSPQERATFISHAN 233
 Db 179 HGDLLNKYLYLSGRVDMRKTEKTIOYLIGSGMDIKSENSPYLGFTYSPQERATFISHAN 238
 OY 234 TAKLAQHYGDKNLAHICGSIASDEKRNHATYTKIVEKLAIEDPDTTVIAPADMRRKRTM 293
 Db 239 TAAQAEHGKIKLAQICGTIAADEKRNHATYTKIVEKLAIEDPDTTVIAPADMRRKRTM 298
 OY 294 PAHLMDGSEDLFKHFTVAORVXYXSALDYCDLIEFLVDKNNVERLTGSLDEGKRAQ 353
 Db 299 PAHLMDGSEDLFKHFTVAORVXYXSALDYCDLIEFLVDKNNVERLTGSLDEGKRAQ 358
 OY 354 YVCELGPKIRVEEKYQKKEKKAEHP--VSFSMFNRELKI 394
 Db 359 YVCELGPKIRVEEKYQKKEKKAEHP--VSFSMFNRELKI 394

RESULT 3

T07806

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - soybean
 N:Alternate names: stearyl-acyl carrier protein desaturase
 C:Species: Glycine max (soybean)
 C>Date: 14-May-1999 #sequence-revision 14-May-1999 #text-change 03-Jun-2002
 C/Accession: T07806

R:Chen, B.Y.; Jones, H.W.
 submitted to the EMBL Data Library, July 1994

A:Reference number: 216145

A:Accession: T07806

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-411 <CHC>

A:Cross-references: EMBL:L34346; NID:g508602; PIDN:AAA92462.1; PID:g508603

C:Genetics:

A:Gene: SACP

A:Genome: nuclear

C:Superfamily: acyl-[acyl-carrier-protein] desaturase

C:Keywords: chloroplast; oxidoreductase

F:1-29/Domain: transit peptide (chloroplast) #status predicted <TNP>

Query Match Best Local Similarity 69.0%; Score 1422.5; DB 2; Length 411;
 Matches 274; Conservative 46; Mismatches 54; Indels 31; Gaps 4;

OY 1 MALKLNFOCKKNHFAFAKSPLEVTFRVSPRVMASTVNSNVLDNLKSP- 51
 Db 1 MALKLN-----PIPGTFLPQMASLRSPFRMASTRSGSEVENIKKPF 46
 OY 52 -----PNQYTHSPPOKLEIFKSLDWMARNVLIHLKSVKSWQPODYLDPVSDGFE 106
 Db 47 TPPEVHVQYTHSPPOKLEIFKSLDWMARNVLIHLKSVKSWQPODYLDPVSDGFE 106
 OY 107 QVRELEKAEIPDDYFVVLVGMITEALPTYSMLNRCDGIDETGAEFSANAMTTRA 166
 Db 107 QVRELEKAEIPDDYFVVLVGMITEALPTYSMLNRCDGIDETGAEFSANAMTTRA 166
 OY 167 WTAENRRHGDLLNKYLYLSGRVDMRKTEKTIOYLIGSGMDIKSENSPYLGFTYSPQERA 226
 Db 167 WTAENRRHGDLLNKYLYLSGRVDMRKTEKTIOYLIGSGMDIKSENSPYLGFTYSPQERA 226
 OY 227 TFIHANTAKLAQHYGDKNLAHICGSIASDEKRNHATYTKIVEKLAIEDPDTTVIAPADM 286
 Db 227 TFIHANTAKLAQHYGDKNLAHICGSIASDEKRNHATYTKIVEKLAIEDPDTTVIAPADM 286
 OY 287 MRKRTPAHLMYDGSDELFKHFTVAORVXYXSALDYCDLIEFLVDKNNVERLTGSLD 346
 Db 287 MRKRTPAHLMYDGSDELFKHFTVAORVXYXSALDYCDLIEFLVDKNNVERLTGSLD 346
 OY 347 EGKRAQEVCELGPKIRVEEKYQKKEKKAEHPVSFSMFNRE 391
 Db 347 EGKRAQEVCELGPKIRVEEKYQKKEKKAEHPVSFSMFNRE 391

RESULT 4

OHC5AD

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - spinach
 N:Alternate names: stearyl-acyl-carrier-protein desaturase
 C:Species: Spinacia oleracea (spinach)
 C>Date: 31-Dec-1992 #sequence-revision 31-Dec-1992 #text-change 03-Jun-2002
 C/Accession: S22480; S18183

R:Nishida, I.; Beppu, T.; Matsuo, T.; Murata, N.
 Plant Mol. Biol. 19, 711-713, 1992
 A:Title: Nucleotide sequence of a cDNA clone encoding a precursor to stearyl-[acyl-c

A:Reference number: S22480; MUID:92329733; PMID:1627785
 A:Accession: S22480

A:Molecule type: mRNA

A:Residues: 1-399 <NTS>

A:Cross-references: EMBL:X62898; NID:g21229; PIDN:CAA44687.1; PID:g21230

C:Superfamily: acyl-[acyl-carrier-protein] desaturase

C:Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase

F:1-35/Domain: transit peptide (chloroplast) #status predicted <TNP>

F:36-399/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match Best Local Similarity 68.4%; Score 1410.5; DB 1; Length 399;
 Matches 273; Conservative 59; Mismatches 55; Indels 19; Gaps 8;

OY 1 MALKLN-----FQCKKNHFAFAKSPLEVTFRVSPRVMASTVNSNVLDNLK--SP 51
 Db 1 MALKLNVPSTPOCKR--LPSPSPROTSPRR--SPKFTMASTLSSSPKAEASTLKKPSP 56

QY	52	P - NLOVTHSMPOKEIFEKSLIDMARNVYIHLKSVKSMQPDQYLPDPVSDSEFEQY	108
		::::: ::::: ::::: ::::: ::::: :::::	
	57	PREVHVYVTHSMPOEKETIEFKSLLEGAEENLVLHLKPVKCMQPDQYLPDPASDEDFQY	116
QY	109	RELREKAKEIPDYFVYLVADMTTEBALPTYSMLRRCGIDKEFGABSAAMMTRAMT	168
		::::: ::::: ::::: ::::: ::::: ::::: :::::	
Db	117	KEIOERAKEIPDOLYVLVADMTTEBALPTYQMLNTLDGAKDEFGASTSAAMVTRAMT	176
QY	169	AEENRHDDLNTKLYLVLSGRVDMRIEKTIOYLLGSGMDIKSENSPYLGEIYVSFOERATF	228
		::::: ::::: ::::: ::::: ::::: ::::: :::::	
Db	177	AEEHRHDDLNTKLYLVLSGRVDMSEIKTIOYLLGSGMDRTENNPYLGEIYVSFOERATF	236
QY	229	ISHANTAKLAQHYGDKNLAHIGSIASDEKRNATATYKIVEKLAETIDPTVYIAFADMKR	288
		::::: ::::: ::::: ::::: ::::: ::::: :::::	
Db	237	VSHNSARLKEHGDJLMAOICIIASDEKRHETATYKIVEKLEFIDPATVIAFADMMK	296
QY	289	KKIMPRHLWDSDELFFHFTFAVAQRYXVSALDYCILEFVLDKNWEVLTJLSDEG	348
		::::: ::::: ::::: ::::: ::::: ::::: :::::	
Db	297	KKISMPRHLWTDGDDMLFHFSAVAQRYXVLTAKYADILEFVLGRMWEVLTJLSSEG	356
QY	349	RKAQYVCGLPRLIRYEEVQOKEKKRKAHEHVSPTWJFNRELKI	394
		::::: ::::: ::::: ::::: ::::: ::::: :::::	
Db	357	OKADQYCSLPKRLRLEER--AREAKQAP-SMPSWJLFDQVU	399

RESULT 5

B39170

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - cucumber

C:Species: Cucumis sativus (cucumber)

C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Jun-2002

C:Accession: B39170

R:Shanklin, J.; Somerville, C.

Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991

A:Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally un-

A:Reference number: A39170; MUID:91172837; PMID:2006187

A:Accession: B39170

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-396 <SHA>

A:Cross-references: GB:M59857

C:Superfamily: acyl-[acyl-carrier-protein] desaturase

C:Keywords: chloroplast; oxidoreductase

Query Match 68.3%; Score 1408; DB 2; Length 396;

Best Local Similarity 66.6%; Pred. No. 3e-95;

Matches 271; Conservative 50; Mismatches 62; Indels 24; Gaps 5;

QY 1 MALKLNFOCKKNHPAFKSPLPVTR-----VSSPRFMASTVNSNVLDNLKSP--- 51

DB 1 MALK-----HPLTSQSKLPSFRMPQLASLNSPKVMASTLSTSEVELLKKPEMP 53

QY 52 ---PMLQVTHSMPPQKLEIFKSLDDMARNNVLHLKSYEKSNQPDYLPDPVSDGFEEOY 108

DB 54 PREVHLQVTHSMPPQKMEIFKSLDDMAEENLVHLKPYERCQPDPLPDSAFEGFHEOY 113

QY 109 RELREKAKELPDYFYVLYVDMITEALPTYMSMLNRCDDGKIDETGAERSSAAMATRAAT 168

DB 114 VELREKAKELPDYFYVLYVDMITEALPTYQTMILNDGVDEFGASPTPAIWRAT 173

QY 169 AENRHGDDLNTKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGIYTSFORATF 228

DB 174 AENRHGDDLNTKLYLSGRVDMRKIEKTIQYLLIGSGMDPRKENNNYLGFIYTSFORATF 223

QY 229 ISHANTAKLAQHTGDKNLAHIGCSIASDEKRNHATAYTIKVELAIEDPTVIAFADMMR 288

DB 234 ISHGNTARLAKHEGDIKLAQICGTITADEKRNHETAYTIKVELAIEDPTVIAFEDMMR 293

QY 289 KKITMPAHNLVQSDSEDLFHNFTAVAAQVRYVYSAIDVCDLLEPLVDKMNVELTGSDSG 348

DB 294 KKVSMPAHNLVQSDRDNLPHHFSVAQRLGVYTIKDVADLLEFLVGRMKVESLTGSGEG 353

QY 349 RKAQEVYCELGPRIKRVEEKVQGEKKKKAEHP-VSFSMIENRELKI 394

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Db      354  QKADYVCAIPARIRKLEERAQGRAK-----EGPTIPFSWIFDRQVKL 396

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RESULT 6

A:acyl-[acyl-carrier-protein] desaturase (BC 1.14.19.2) precursor - safflower
C:Species: *Carthamus tinctorius* (safflower);
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C:Accession: A39173
R:Thompson, G.A.; Scherer, D.E.; Foxall-Van Aken, S.; Kenny, J.W.; Young, H.L.; Shultz
Proc. Natl. Acad. Sci. U.S.A. 88, 2578-2582, 1991
A:Title: Primary structures of the precursor and mature forms of stearyl-acyl carrier
A:Reference number: A39173; MUID:91172850; PMID:2006194
A:Accession: A39173
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-396 <THO>
A:Cross-references: GB:661109; NID:g167196; PID:AAA3021.1; PID:g167197
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase

Query MatchSimilarity	68.2%	Score 1406	DB 1	Length 396
Best Local Similarity	67.1%	Pred. No. 4	2e-95	
Matches 271	Conservative 54	Mismatches 61	Indels 18	Gaps 5

[illegible]

RESULT 7

acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - turnip
C:Species: Brassica rapa (turnip)
C:Date: 22-Nov-1993 #sequence,revision 10-Nov-1995 #text,change 03-Jun-2002
C:Accession: S23351
R:Knutzon, D.S.; Thompson, G.A.; Radke, S.E.; Johnson, W.B.; Knauf, V.C.; Kridl, J.C.
Proc. Natl. Acad. Sci. U.S.A. 89, 2624-2628, 1992
A:Title: Modification of Brassica seed oil by acyltransferase expression of a stearyl-acyl
A:Reference number: S23351; MUID:92212881; PMID:1557366
A:Accession: S23351
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-398 <KNU>
A:Cross-references: EMBL:X60978; NID:g17928; PIDN:CAA3294.1; PID:g17929
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
:Keywords: chloroplast; oxidoreductase

Query Match	Best Local Similarity	67.7%	Score 1396;	DB 2;	Length 398;
Matches 26;	Conservative 55;	Mismatches 66;	Indels 12;	Gaps 4;	
QY	1	MALKLNFOCKK -NHPAAFASPLPYTRASSPVFMASTVNSWVLNDNLSKSP-----P	52		
DB	1	MAUKLNELASQPNFNPSS-ARPIISIFRSPKFLCLANSSSALSSKEVESLKKFFTPPEKY	59		
QY	53	NLOVTHSPPOKLEIFRSLDDMARNNVLIHLKSVESKSWOPDYLPPVSDGEEQYRELR	112		
DB	60	HVOVLNMPPOKLEIFKSMEDMAEONILTLQKVEKSWOPDPLPPASDGFEDQYRELR	119		
QY	113	ERAKETPDVYFVVLVGDMLTEALPTFYMSLNCDGDKQETGEPASAMMTRAMTAEN	172		
DB	120	ERARELPEDYFVVLVGDMLTEALPTQYMLNLTDVQRETSASPSMAITRAMTAEN	179		
QY	173	RHDDLNLNKYLYSGRDMRKIEKTYOYLIGSGMDIKSENSPYLGFIYTSFOERATFISHA	232		
DB	180	RHDDLNLNKYLYSGRDMQOIEKTYOYLIGSGMDPTENNPGLGFIYTSFOERATFISHG	239		
QY	233	NTAKLAQHGDKNLAIIGCSIASDEKRRHATATKYIEKAEILDPDPTVYAFADMRRKIT	292		
DB	240	NTARQAKHEGDLKLAQIGCTIADDERHETATKYIEKLEFLDPDPTVYAFADMRRKIS	299		
QY	293	MPAHMLYDSSDELFRHFTAAVAAQXXVYSALDYCDLLEFLYDKMNVERTLSDSGRKAQ	352		
DB	300	MPAHMLYDRDSESLFENFSSVAORGVYTAQYADILEFLYGRMKITESTLTGSGGNKAQ	359		
QY	353	EYVCELPKIRRVEEKVQGEKKKKAHEHPSWTFNNEPKI	394		
DB	360	EYICGLTPRIRRLDEAQAARAKGP---KVPESWJHDEVOVL	398		

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RESULT 8
T14264
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower
M:Alternate names: stearyl-ACP desaturase
C:Species: Helianthus annuus (common sunflower)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T14264
R:Hongtrakul, V., Slabaugh, M.B., Knapp, S.J.
submitted to the EMBL Data Library, February 1997
A:Description: Sunflower stearoyl-ACP desaturase.
A:Reference number: Z17946
A:Accession: T14264
A:Status: preliminary; translated from GB/EMBL/DBDUT
A:Molecule type: mRNA
A:Residues: 1-396 <HON>
A:Cross-references: EMBL:U91339, NID:g2290399, PID:g2290400
A:Experimental source: Strain Mammoth
C:Function:
A:Description: Introduces a double bond at the delta(9) position of stearoyl-ACP generated
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: fatty acid biosynthesis; oxidoreductase

Query Match          67.7%; Score 1395; DB 2; Length 396;
Best Local Similarity 66.9%; Pred. No. 2.7e-94;
Matches 267; Conservative % 52; Mismatches 56; Indels 24; Gaps 4;

QY 16 AFAKSPLPVTR-----VSSRYVMASTVNSNSKVLNDNLKSP-----PMLQV 56
   | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 2 ALRMSPVTLQREIYPSTFHOSKNLRSPKRFMAASTIGSSIPKVSFTKPFPPREHVH 61

QY 57 THSPMPKLEIFKSLDDMARNNVLHLEKSVKSNQOPDYPDPVSDGFEQVRELRERAK 116
   |||||:||||: | :|:|:| | | | | | | | | | | | | | | | | |
Db 62 THSPMPKRIETFKSEIGMAEDNLIHLKPYDKCKQPPDLELPASDSGFEQVKELRARAK 121

QY 117 EIPDDYVNVLVGDMITEALPTYSMLNRCDGIKDETGAEPSAWAMTRAWTAENHGD 176
   |||||:|||||:| | | | | | | | | | | | | | | | | |
Db 122 EIPDEYVNVLVGDMITEALPTVOTMLNTLIDGVDEFGASPTPAWIMTRAWTAENHGD 181

QY 177 LNKVYILSGRVDMRKTEKTIQVLIGSGMDIKSNSTYLGFIITSFQERRFTISHANTAK 236

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Db	182	LAHQYDLYLSGRVADMOIQIOTIYLLGSGMDERTENSPILGFIYTSFQERATFISHGNTAR	241
QY	237	LAOHVDDKMLAHGCSIASDERKHNATATKIVKIAIEDPPTYIARADMKRKITMPAR	296
Db	242	HKNDYODLKLACIGSTIAADEKRHETATTKIAEKLFIEDPCGYLAADMKRKITSMPAR	301
QY	297	LMTDGSDELLKHNPTAVAQRYXVSALDYCDLLEFLYDKMNVERTLTSLDSEGRKAEYVC	356
Db	302	LMYDGRDDLDLFHFSAVAOBRLGVYAKYADILBEFLYGRMKVADULTSLSEGRKADYVC	361
QY	357	ELGPKIRRYEEKVQGEKKKKAENH-VSFSTIRNRELKI	394
Db	362	GLPSRIKRLREBAARAK----EGDSLPFSMIFREVKL	396

RESULT 9
 S44202
 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - Commerson's wild po
 N:Alternate names: stearyl-ACP desaturase
 C:Species: Solanum commersonii (Commerson's wild potato)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Jun-2002
 C:Accession: S44202
 R:Ritucci, M.; Grillo, S.; Costa, A.; Leone, A.
 submitted to the EMBL Data Library, April 1994
 A:Reference number: S44202
 A:Accession: S44202
 A:Molecule type: mRNA
 A:Residues: 1-393 <TRU>
 A:Cross-references: EMBL:X78935; NID:g474832; PIDN:CAA5535.1; PID:g474833
 C:Genetics:
 A:Genome: nuclear
 C:Superfamily: acyl-[acyl-carrier-protein] desaturase
 C:Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase
 E:1-30/Domain: transit peptide (chloroplast) #status predicted <TRP>
 F:31-393/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

[illegible]

[illegible]

[illegible]

RESULT 13
T14268
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower
N:Alternate names: stearoyl-ACP desaturase
C:Species: *Helianthus annuus* (common sunflower)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T14268
R:Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J.
submitted to the EMBL Data Library, February 1997
A:Description: Sunflower stearoyl-ACP desaturase.
A:Reference number: Z17946

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-396 <HON>
A:Cross-references: EMBL:U91340; NID:g22290401; PID:g22290402
A:Experimental source: strain Mammoth
C:Function:
A:Description: introduces a double bond at the delta(9) position of steroyl-ACP generated
C:Pathway: fatty acid biosynthesis
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: fatty acid biosynthesis; oxidoreductase

Query Match	67.0%	Score 1381;	DB 2;	Length 396;
Best Local Similarity	66.58%	Pred. No. 2.8e-93;		
Matches 268; Conservative	54;	Mismatches 65;	Indels 16;	Gaps 5.

[illegible]

RESULT 14
T10793
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - upland cotton
N;Alternate names: delta 9 stearoyl-[acyl-carrier protein] desaturase

C:Species: *Gossypium hirsutum* (upland cotton)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: F10793
R: Liu, Q.; Singh, S.; Sharp, P.; Green, A.; Marshall, D.R.
Plant Physiol. 110, 1436, 1996
A:Title: Nucleotide sequence of a cDNA from *Gossypium hirsutum* encoding a stearyl-ac
A:Reference number: Z17148
A:Accession: F10793
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-397 <LTI>
A:Cross-references: EMBL:X95988; NID:91217627
A:Experimental source: cultivar deltapipe-16
C:Function:
A:Description: introduces a double bond at the delta(9) position of stearyl-ACP gene
A:Pathway: fatty acid biosynthesis
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: fatty acid biosynthesis; oxidoreductase; unsaturated fatty acid biosynthe
E:1-65/Domain: signal sequence #status predicted <SIG>
E:66-397/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match	66.7%;	Score 1375.5;	DB 2;	Length 397;
Best Local Similarity	67.7%;	Pred. No. 7.1e-93;		
Matches 272;	Conservative 41;	Mismatches 76;	Indels 13;	Gaps 6;

QY	1	MAK1NFQCKNNH--AAFAKSPLEPVTRSRSPRYVMATVNSNVLNKK---SPV---	53
Db	1	MA1NFMA1ASQQLPCFALPRAKTLR--SPKSMISTIT1SGSKSEVGNLKKRPFLPREVP	58
QY	54	LQVTHSMPPKRLTE1FKSLDDWANNVL1HLKSVKSNQPODYLPPDPVSDGFEEQVRELR	113
Db	59	VO1THSMPPKHTE1FKSLDEGAENNN1LHLKRVKSCQPADFLPPDPVSDGFEEQVRELR	118
QY	114	RAKE1PDDYFVVLVGMITEALETTYSMLNRCDGIDDEFGAESNAAMTTRAVTAENR	173
Db	119	RAKE1PDDYFVVLVGMITEALETSTYOTMLNTLDGTDEFGASLTLPMAITRAVTAENR	178
QY	174	HGDL1NNYLYLGSVDMRK1EKTQVYL1GSGMD1KSNNSYLG1TNSPDEBRTAF1SHAN	233
Db	179	HGDL1NNYLYLGSVDMRKQ1ERTQVYL1GSGMDHNTNSP1RG1TNSPDEBRTAF1SHGN	238
QY	234	TAK1LAOHYGDKNLH1IGSG1ASDEKRAHATYATK1VEK1AE1EDPTVY1APADMMKRKT1TM	293
Db	239	TGR1AKETGQD1NLQ1IGSG1ASDEKRIHEATYATK1VEK1LE1FDPELY1ALADMMKK1IAM	298
QY	294	PAHLMDGSDLE1FKHFTTAAQRVXYV1SALDYCD1LEFLVDKNVVERLT1G1SDGKKAQF	353
Db	299	PAEFLYDGRDYN1LPDHYSAVAQR1GCVYTAQDYVD1EHLVDNRKVKTEL1G1SDEGKRAQD	358
QY	354	YVCELGPKIR1RVEKVOGKEKKKAHEPVS--FSV1NFNRKELK1	394
Db	359	Y1CS1PSR1R1RLERRAQ---EKAGGSP1RVSF1S1F1PREVK1	397

RESULT 15
T14172
acyl-fatty-carrier-protein) desaturase (EC 1.14.19.2) - common sunflower
N:Alternate names: stearoyl-ACP desaturase
C:Species: Helianthus annuus (common sunflower)
C:Date: 20-Sep-1999 #sequence-revision 20-Sep-1999 #text-change 03-Jun-2002
C:Accession: T14172
R:Coughlan, S.J.; Hastings, C.E.; Winfrey, R.J.
Submitted to the EMBL Data Library, September 1996
Description: Sunflower stearoyl-ACP desaturase.

A:Accession: T14172 translated from GB/EMBL/DBJ
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1 396 <CRU>
A:Cross-references: EMBL:U70374; NID:G1575696; PID:G1575697
A:Experimental source: strain SMF3
C:Function:
C:Description: Introduces a double bond at the delta(9) position of steryl-ACP gene

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OM protein - protein search, using sw model

Run on: December 1, 2002, 21:19:31 ; Search time 18 Seconds

(without alignments)
644.035 Million cell updates/sec

Title: us-09-732-597-2

Perfect score: 2062

Sequence: 1 MALKLNPOCKKNHPAFAK.....KKAEHPVSFWFRELKI 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1544.5	74.9	385	1 US-08-539-798-4	Sequence 4, Appli
2	1544.5	74.9	385	1 US-08-328-560-4	Sequence 4, Appli
3	1490	72.3	396	1 US-08-539-798-3	Sequence 3, Appli
4	1490	72.3	396	1 US-08-329-560-3	Sequence 3, Appli
5	1490	72.3	396	1 US-08-471-791-16	Sequence 16, Appli
6	1490	72.3	396	4 US-08-926-522-4	Sequence 4, Appli
7	1490	72.3	396	5 PCT-US91-01746-16	Sequence 16, Appli
8	1436.5	69.7	391	1 US-07-995-657-6	Sequence 6, Appli
9	1436.5	69.7	391	1 US-08-474-587-6	Sequence 6, Appli
10	1406	68.2	396	1 US-08-471-791-13	Sequence 13, Appli
11	1406	68.2	396	4 US-08-926-522-2	Sequence 2, Appli
12	1406	68.2	396	5 PCT-US91-01746-13	Sequence 13, Appli
13	1396	67.7	398	1 US-08-471-791-30	Sequence 20, Appli
14	1396	67.7	398	4 US-08-926-522-6	Sequence 6, Appli
15	1396	67.7	398	5 PCT-US91-01746-20	Sequence 20, Appli
16	1174.5	57.0	368	2 US-08-869-137-2	Sequence 2, Appli
17	1106	53.6	387	1 US-08-539-798-2	Sequence 2, Appli
18	1106	53.6	387	1 US-08-329-560-2	Sequence 2, Appli
19	278	13.5	54	3 US-08-917-299-19	Sequence 19, Appli
20	278	13.5	54	4 US-09-422-662-19	Sequence 19, Appli
21	261	12.7	52	4 US-08-917-299-34	Sequence 34, Appli
22	261	12.7	52	4 US-09-422-662-34	Sequence 34, Appli
23	255	12.4	338	3 US-08-917-299-4	Sequence 4, Appli
24	255	12.4	338	3 US-08-917-299-37	Sequence 37, Appli
25	255	12.4	338	4 US-09-422-662-4	Sequence 4, Appli
26	255	12.4	338	4 US-09-422-662-37	Sequence 37, Appli
27	253	12.3	54	3 US-08-917-299-12	Sequence 12, Appli

28	253	12.3	54	3 US-08-917-299-16	Sequence 16, Appli
29	253	12.3	54	4 US-09-422-662-12	Sequence 12, Appli
30	253	12.3	54	4 US-09-422-662-16	Sequence 16, Appli
31	252	12.2	54	3 US-08-917-299-15	Sequence 15, Appli
32	252	12.2	54	4 US-09-422-662-15	Sequence 15, Appli
33	251	12.2	54	3 US-08-917-299-13	Sequence 13, Appli
34	251	12.2	54	4 US-08-917-299-13	Sequence 13, Appli
35	241	11.7	54	3 US-08-917-299-18	Sequence 18, Appli
36	241	11.7	54	4 US-09-422-662-18	Sequence 18, Appli
37	241	11.7	56	1 US-08-471-791-2	Sequence 2, Appli
38	241	11.7	56	5 PCT-US91-01746-2	Sequence 2, Appli
39	238	11.5	54	3 US-08-917-299-13	Sequence 13, Appli
40	238	11.5	54	4 US-09-422-662-17	Sequence 17, Appli
41	236	11.4	54	3 US-08-917-299-14	Sequence 14, Appli
42	236	11.4	54	4 US-09-422-662-14	Sequence 14, Appli
43	232	11.3	57	1 US-08-471-791-7	Sequence 7, Appli
44	232	11.3	57	5 PCT-US91-01746-7	Sequence 7, Appli
45	216	10.5	52	3 US-08-917-299-33	Sequence 33, Appli

ALIGNMENTS

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RESULT 1
US-08-539-798-4
; Sequence 4, Application US/08539798
; Patent No. 5614400
; GENERAL INFORMATION:
; APPLICANT: CAHOON, Edgar B.
; TITLE OF INVENTION: Methods and Compositions Relating to
; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: US
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,798
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,560
; FILING DATE: 26-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Yates, Michael E.
; REGISTRATION NUMBER: 36,063
; REFERENCE/DOCKET NUMBER: 0284US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-539-798-4
;
; Query Match 74.9%; Score 1544.5; DB 1; Length 385;
; Best local Similarity 73.1%; Pred. No. 2.2e-148;
; Matches 296; Conservative 42; Mismatches 36; Indels 31; Gaps 5;
;
; 1 MALKLN-----FOCKKNHPAFAKSPLEPVTVRVSSP-----RVPMASIVNSNSWLDNKK 49
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Db      1 MAMKLNALMTLQCPKRN-----MFTRIAPPOAGRVRSKVSMASTLHASPLVFEDK 51
QY      50 SPNNIQTHTSNMPQKLEIFKSLDDMARNNVLIHKSVKSWQPODYLDPDVSDFGEQVR 109
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Db      52 AG-----RPEVDELFNLSLEGWARDNITLVHLKSVENSWQPODYLDPDVSDFGEQVR 102
QY      110 ELERAKELIPDDYFVYLVGDMITEEALPTVMSMLNRCDGKIDETGAPPSAMAMTRAWTA 169
      :      :      :      :      :      :      :      :      :      :      :
Db      103 EMERKADIPDEFYVYLVGDMITEEALPTVMSMLNRCDGKIDETGAPPSAMAMTRAWTA 162
QY      170 EENRHGDLNKKYLLYLSGRVDMRIEKTQYLLIGSGMDIKSENSPYLGFYTSFQERATFI 229
      :      :      :      :      :      :      :      :      :      :      :
Db      163 EENRHGDLNKKYLLYLSGRVDMRIEKTQYLLIGSGMDIKSENSPYLGFYTSFQERATFI 222
QY      230 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATAYTKIVEKLAIEDPPTVIAFADMMRK 289
      :      :      :      :      :      :      :      :      :      :      :
Db      223 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATAYTKIVEKLAIEDPPTVIAFADMMRK 282
QY      290 KITMPAHLMYDGSDELFRKHTFAVQRYVXSALDYCDILEFLVDKNVVERLTGSLDEGR 349
      :      :      :      :      :      :      :      :      :      :      :
Db      283 KIOMPAHAMYDGSDDLFRKHTFAVQRYVXSALDYCDILEFLVDKNVVERLTGSLDEGR 342
QY      350 KAOEYVCGLGPKIRVEEKVQGEKKKAHEHVSFSWIFNRRLKI 394
      :      :      :      :      :      :      :      :      :      :      :
Db      343 KAOEYVCSLAAKIRVEEKVQGE--KRAVLPAVAFSWIFNRROI 385

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RESULT 2

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US-08-329-560-4
; Sequence 4, Application US/08329560
; Patent No. 5654402
; GENERAL INFORMATION:
; APPLICANT: CAHOON, Edgar B.
; TITLE OF INVENTION: Methods and Compositions Relating to
; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: US
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,560
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Yates, Michael E.
; REGISTRATION NUMBER: 36,063
; REFERENCE/DOCKET NUMBER: 02840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-329-560-4

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Query Match      74.9%; Score 1544.5; DB 1; Length 385;
Best Local Similarity 73.1%; Pred. No. 2.2e-148;
Matches 296; Conservative 42; Mismatches 36; Indels 31; Gaps 5;
QY      1 MALKLN----FOCKKNHPAFAKSLPVTYVSSP-----RVFASATYNSNSMWLDNLK 49

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Db      1 MAMKLNALMTLQCPKRN-----MFTRIAPPOAGRVRSKVSMASTLHASPLVFEDK 51
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Db      52 AG-----RPEVDELFNLSLEGWARDNITLVHLKSVENSWQPODYLDPDVSDFGEQVR 102
QY      110 ELERAKELIPDDYFVYLVGDMITEEALPTVMSMLNRCDGKIDETGAPPSAMAMTRAWTA 169
      :      :      :      :      :      :      :      :      :      :      :
Db      103 EMERKADIPDEFYVYLVGDMITEEALPTVMSMLNRCDGKIDETGAPPSAMAMTRAWTA 162
QY      170 EENRHGDLNKKYLLYLSGRVDMRIEKTQYLLIGSGMDIKSENSPYLGFYTSFQERATFI 229
      :      :      :      :      :      :      :      :      :      :      :
Db      163 EENRHGDLNKKYLLYLSGRVDMRIEKTQYLLIGSGMDIKSENSPYLGFYTSFQERATFI 222
QY      230 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATAYTKIVEKLAIEDPPTVIAFADMMRK 289
      :      :      :      :      :      :      :      :      :      :      :
Db      223 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATAYTKIVEKLAIEDPPTVIAFADMMRK 282
QY      290 KITMPAHLMYDGSDELFRKHTFAVQRYVXSALDYCDILEFLVDKNVVERLTGSLDEGR 349
      :      :      :      :      :      :      :      :      :      :      :
Db      283 KIOMPAHAMYDGSDDLFRKHTFAVQRYVXSALDYCDILEFLVDKNVVERLTGSLDEGR 342
QY      350 KAOEYVCGLGPKIRVEEKVQGEKKKAHEHVSFSWIFNRRLKI 394
      :      :      :      :      :      :      :      :      :      :      :
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RESULT 3

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US-08-539-798-3
; Sequence 3, Application US/08539798
; Patent No. 5614400
; GENERAL INFORMATION:
; APPLICANT: CAHOON, Edgar B.
; TITLE OF INVENTION: Methods and Compositions Relating to
; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: US
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,798
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,560
; FILING DATE: 26-Oct-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Yates, Michael E.
; REGISTRATION NUMBER: 36,063
; REFERENCE/DOCKET NUMBER: 02840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-539-798-3

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Query Match      72.3%; Score 1490; DB 1; Length 396;

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Best Local Similarity 71.1%; Pred. No. 8e-143;
Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

QY 1 MALKLN-FOCKKHPAAFAKSPLEPVTVSSPRVFMASSTVNSMVLNKLSP-----PN 53
1 MALKLNFLSQTKLPSPALPMASTR--SPKFTMASTLKSCKSEVENLKKRPMPPREYH 58
QY 54 LQVTHSPPOKLEIFKSLDMMARNVLIHLKSVESKMOPODLPDPVSDGFEQVRELE 113
59 VQVTHSPPOKLEIFKSLDMMARNVLIHLKSVESKMOPODLPDPVSDGFEQVRELE 118
QY 114 RAKEIPDDYFVVLVGMDEALPTYQTMNLTDGVRDEFGASPTSMALWTAMTAENR 173
119 RAKEIPDDYFVVLVGMDEALPTYQTMNLTDGVRDEFGASPTSMALWTAMTAENR 178
QY 174 HGDLLNKYLYLSGRVMDRIEKTQYLLIGSGMDIKSENSPYLGFTYTSFOERATFISHN 233
179 HGDLLNKYLYLSGRVMDRIEKTQYLLIGSGMDIKSENSPYLGFTYTSFOERATFISHN 238
QY 234 TAKLAQHYGDKNLAHICGSIASDEKRRHATYTKIVEKLAIEDPTTVIAFADMMRKKT 293
239 TARQAKHEGDIKLAQICGTLADEKRHEATYTKIVEKLEIDPDGTVLAFADMMRKKT 298
QY 294 PAHLMYDGSDELLFKHFTAVAQRYVXSALDYCDLLEFLVDMKNVERLTGLSDEGRKAOE 353
299 PAHLMYDGRDNLDFHFSAAQRLGVYAKDYADLLEFLVGRMKVKDLTGLSDEGRKAOE 358
QY 354 YVCELGPRTIRVEEKVQGEKKKAEHP--VSFSMTINRELKI 394
359 YVCLRPRIIRLERAEGRAK----EAPTMPFSMTIDROVKL 396

Db

RESULT 4
US-08-329-560-3
; Sequence 3, Application US/08329560
; Patent No. 5654402
; GENERAL INFORMATION:
; APPLICANT: CAHOON, Edgar B.
; APPLICANT: OHLGROE, John B.
; TITLE OF INVENTION: Methods and Compositions Relating to
; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: US
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/329,560
; FILING DATE: 26-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Yates, Michael E.
; REGISTRATION NUMBER: 36,063
; REFERENCE/DOCKET NUMBER: 0284US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-329-560-3

Query Match 72.3%; Score 1490; DB 1; Length 396;
Best Local Similarity 71.1%; Pred. No. 8e-143;
Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

QY 1 MALKLN-FOCKKHPAAFAKSPLEPVTVSSPRVFMASSTVNSMVLNKLSP-----PN 53
1 MALKLNFLSQTKLPSPALPMASTR--SPKFTMASTLKSCKSEVENLKKRPMPPREYH 58
QY 54 LQVTHSPPOKLEIFKSLDMMARNVLIHLKSVESKMOPODLPDPVSDGFEQVRELE 113
59 VQVTHSPPOKLEIFKSLDMMARNVLIHLKSVESKMOPODLPDPVSDGFEQVRELE 118
QY 114 RAKEIPDDYFVVLVGMDEALPTYQTMNLTDGVRDEFGASPTSMALWTAMTAENR 173
119 RAKEIPDDYFVVLVGMDEALPTYQTMNLTDGVRDEFGASPTSMALWTAMTAENR 178
QY 174 HGDLLNKYLYLSGRVMDRIEKTQYLLIGSGMDIKSENSPYLGFTYTSFOERATFISHN 233
179 HGDLLNKYLYLSGRVMDRIEKTQYLLIGSGMDIKSENSPYLGFTYTSFOERATFISHN 238
QY 234 TAKLAQHYGDKNLAHICGSIASDEKRRHATYTKIVEKLAIEDPTTVIAFADMMRKKT 293
239 TARQAKHEGDIKLAQICGTLADEKRHEATYTKIVEKLEIDPDGTVLAFADMMRKKT 298
QY 294 PAHLMYDGSDELLFKHFTAVAQRYVXSALDYCDLLEFLVDMKNVERLTGLSDEGRKAOE 353
299 PAHLMYDGRDNLDFHFSAAQRLGVYAKDYADLLEFLVGRMKVKDLTGLSDEGRKAOE 358
QY 354 YVCELGPRTIRVEEKVQGEKKKAEHP--VSFSMTINRELKI 394
359 YVCLRPRIIRLERAEGRAK----EAPTMPFSMTIDROVKL 396

Db

RESULT 5
US-08-471-791-16
; Sequence 16, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knaut, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762,762
; FILING DATE: 16-SEPT-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 69-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-791-16

Query Match 72.3%; Score 1490; DB 1; Length 396;
Best Local Similarity 71.1%; Pred. No. 8e-143;
Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

QY 1 MALKLN-FOCKKNHPAAFAKSPLEPTRVSSPRVFMASTVNSNSMVLNLSKSP-----PN 53
Db 1 MALKLNPLFSQOTOKLPSEFALPPMASTR--SPKFFYMASTLKSQSKSEVENLKKPPMPREH 58
QY 54 LOVTHSMPPQKLEIFKSLDMDARNVNLHLKSVKSWOPQDYLDPDVSQGFEEVRELRE 113
Db 59 VOVTHSMPPQKLEIFKSLDMDARNVNLHLKSVKSWOPQDYLDPDVSQGFEEVRELRE 118
QY 114 RAKEIPDDYFVVLVGDMLTEALPTVMSLNRCDGKIDETGAPSPAMAMTRAMTAENR 173
Db 119 RAKEIPDDYFVVLVGDMLTEALPTVMSLNRCDGKIDETGAPSPAMAMTRAMTAENR 178
QY 174 HGDLNKKLYLISGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFOERATFTISHN 233
Db 179 HGDLNKKLYLISGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFOERATFTISHN 238
QY 234 TAKLAQHGDKNLAHICGSIASDEKRHATAYTKIVEKLAIEDPDTTVIAFADMMRRKKT 293
Db 239 TARQAKHEHDDIKLAQICGIIADDEKRHETAYTKIVEKLEIDPDGTVLAFADMMRRKKT 298
QY 294 PAHLMYDGSDELLFKHFTVAQVRVYVSALDYCDILEFLVDKWNVERLTGLSDEGRKAOE 353
Db 299 PAHLMYDGRDNLDFHFSVAQRLGYTAKDYADILEFLVGRKVKDKLTGLSDEGRKAOE 358
QY 354 YVCELGPKIRIRVEEKVQGEKKKAHP--VSFSWIFNRELKI 394
Db 359 YVCRLLPPIRIRLEERAQGRAK----EAPTMPFSWIFDROVKL 396

RESULT 6
US-08-926-522-4
Sequence 4, Application US/08926522
Patent No. 6426447
GENERAL INFORMATION:
APPLICANT: Vic C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: PLANT SEED OILS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,522
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,173
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE DES
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-926-522-4

Query Match 72.3%; Score 1490; DB 4; Length 396;
Best Local Similarity 71.1%; Pred. No. 8e-143;
Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

QY 1 MALKLN-FOCKKNHPAAFAKSPLEPTRVSSPRVFMASTVNSNSMVLNLSKSP-----PN 53
Db 1 MALKLNPLFSQOTOKLPSEFALPPMASTR--SPKFFYMASTLKSQSKSEVENLKKPPMPREH 58
QY 54 LOVTHSMPPQKLEIFKSLDMDARNVNLHLKSVKSWOPQDYLDPDVSQGFEEVRELRE 113
Db 59 VOVTHSMPPQKLEIFKSLDMDARNVNLHLKSVKSWOPQDYLDPDVSQGFEEVRELRE 118
QY 114 RAKEIPDDYFVVLVGDMLTEALPTVMSLNRCDGKIDETGAPSPAMAMTRAMTAENR 173
Db 119 RAKEIPDDYFVVLVGDMLTEALPTVMSLNRCDGKIDETGAPSPAMAMTRAMTAENR 178
QY 174 HGDLNKKLYLISGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFOERATFTISHN 233
Db 179 HGDLNKKLYLISGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFOERATFTISHN 238
QY 234 TAKLAQHGDKNLAHICGSIASDEKRHATAYTKIVEKLAIEDPDTTVIAFADMMRRKKT 293
Db 239 TARQAKHEHDDIKLAQICGIIADDEKRHETAYTKIVEKLEIDPDGTVLAFADMMRRKKT 298
QY 294 PAHLMYDGSDELLFKHFTVAQVRVYVSALDYCDILEFLVDKWNVERLTGLSDEGRKAOE 353
Db 299 PAHLMYDGRDNLDFHFSVAQRLGYTAKDYADILEFLVGRKVKDKLTGLSDEGRKAOE 358
QY 354 YVCELGPKIRIRVEEKVQGEKKKAHP--VSFSWIFNRELKI 394
Db 359 YVCRLLPPIRIRLEERAQGRAK----EAPTMPFSWIFDROVKL 396

RESULT 7
PCT-US91-01746-16
Sequence 16, Application PC/TUS9101746
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases -Compositions and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.


```

: STREET: 1920 Fifth Street
: CITY: Davis
: STATE: California
: COUNTRY: USA
: ZIP: 95616
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 6.0.7
: SOFTWARE: Microsoft Word 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/01746
: FILING DATE: 19910314
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/615,784
: FILING DATE: 14-NOV-1990
: APPLICATION NUMBER: 07/567,373
: FILING DATE: 13-AUG-1990
: APPLICATION NUMBER: 07/494,106
: FILING DATE: 16-MAR-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Lassen, Elizabeth
: REGISTRATION NUMBER: 31,845
: NAME: Donna E. Scherer
: REGISTRATION NUMBER: 34,719
: REFERENCE/DOCKET NUMBER: CGNE 69-3.WO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (916) 753-6313
: TELEFAX: (916) 753-1510
: TELEX: 350370 CGNE
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 396 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US91-01746-16
:
: Query Match
: Best Local Similarity 71.1%; Pred. No. 8e-143;
: Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;
:
: QY 1 MALKLN-FQCKKKNHRAAKSPLPVTRVSSPRVFMATVNSNVMNLNLSKSP-----PN 53
:   1 MALKLNPFLOQKLPSPALPPEMASTR--SPKRYMASTLKSKEVENLKKPEMPREVA 58
:
: QY 54 LQVTHSMFPQKLEIFKSLDDMARNNVLIHLKSEKSMQPODYLPDPVSDGFEEQVELKE 113
:   59 VQVTHSMFPQKLEIFKSLDDMARNNVLIHLKSEKSMQPODYLPDPVSDGFEEQVELKE 118
:
: QY 114 RAKELPDDYFVVLVGDMTTEALPTYMSMLNRCDGIDETGAEPSSAMWMTAENR 173
:   119 RAKELPDDYFVVLVGDMTTEALPTYQTMNLTDGVRDGTGASPTSWAINTWMTAENR 178
:
: QY 174 HGDLNLKLYLSGRVDMRKIEKTIQYILGSGMDIKSENSPYLGFIYTSFOERATFTSHAN 233
:   179 HGDLNLKLYLSGRVDMRKIEKTIQYILGSGMDIPRENSPYLGFIYTSFOERATFTSHGN 238
:
: QY 234 TAKLQNHGDKRLAHICGSIASDEKRNATATYTKIYEKLALEIDPDTTVIAFADMRKKITM 293
:   239 TARQKKEGDKLQAOICGFIADKRNHETATYTKIYEKLEIDPDGTVLAFADMRKKISN 298
:
: QY 294 PAHLVDSDELLEFKHFTVAORVXYVSALDYCDLLEFLVDKMNVERLTGLSDEGRKAOE 353
:   299 PAHLVDSDELLEFKHFTVAORVXYVSALDYCDLLEFLVDKMNVERLTGLSDEGRKAOE 358
:
: QY 354 YVCELGPKIRVEEKVQCKRKKAEHP--VSESWIFNRELKI 394
:   359 YVCELGPKIRVEEKVQCKRKKAEHP--VSESWIFNRELKI 396
:
: RESULT 8
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: US-07-995-657-6
: Sequence 6, Application US/07995657
: Patent No. 5443974
: GENERAL INFORMATION:
: APPLICANT: Hiltz, William D.
: APPLICANT: Yadav, Narendra S.
: APPLICANT: Perez, Grau, Luis
: TITLE OF INVENTION: Nucleotide Sequence of
: TITLE OF INVENTION: Soybean Stearoyl-ACP
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: E. I. du Pont de Nemours
: ADDRESSEE: and Company
: STREET: 1007 Market Street
: CITY: Wilmington
: STATE: Delaware
: COUNTRY: U.S.A.
: ZIP: 19898
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
: COMPUTER: Macintosh
: OPERATING SYSTEM: Macintosh System, 6.0
: SOFTWARE: Microsoft Word, 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/995,657
: FILING DATE: 19921211
: FILING DATE: C) CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: GEIGER, KATHLEEN W.
: REGISTRATION NUMBER: 35,880
: REFERENCE/DOCKET NUMBER: BB_1022-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 302-892-8112
: TELEFAX: 302-892-7949
: TELEX: 835420
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 391 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: unknown
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-995-657-6
:
: Query Match
: Best Local Similarity 69.7%; Score 1436.5; DB 1; Length 391;
: Matches 278; Conservative 44; Mismatches 53; Indels 31; Gaps 4;
:
: QY 1 MALKLN-FQCKKKNHRAAKSPLPVTRVS-----SPRVFMATVNSNVMNLNLSKSP- 51
:   1 MALKLN-----PIPTQTFSLPQMPSLRSPREFMASTLKSKEVENIKRPF 46
:
: QY 52 -----PLQVTHSMFPQKLEIFKSLDDMARNNVLIHLKSEKSMQPODYLPDPVSDGFE 106
:   47 TPPEVNVQVTHSMFPQKLEIFKSLDDMARNNVLIHLKSEKSMQPODYLPDPVSDGFE 106
:
: QY 107 QVRELRAKEIPDDYFVVLVGDMTTEALPTYMSMLNRCDGIDETGAEPSSAMWMTA 166
:   107 QVRELRAKEIPDDYFVVLVGDMTTEALPTYQTMNLTDGVRDGTGASPTSWAINTW 166
:
: QY 167 WTAENRHGDLNLKLYLSGRVDMRKIEKTIQYILGSGMDIKSENSPYLGFIYTSFOERA 226
:   167 WTAENRHGDLNLKLYLSGRVDMRKIEKTIQYILGSGMDIPRENSPYLGFIYTSFOERA 226
:
: QY 227 TFSHGNTARLAKENHGKIKLAQICGMTASDEKRNHETATYTKIYEKLEFVDPDGTMAAD 286
:   227 TFSHGNTARLAKENHGKIKLAQICGMTASDEKRNHETATYTKIYEKLEFVDPDGTMAAD 286
:
: QY 287 MRKKITMPAHLMDGSDLELFKHFTVAORVXYVSALDYCDLLEFLVDKMNVERLTGLSD 346
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Db 287 MRKTIAMPALMYDGRDNLFDNYSVAORIGVYTAQADIDLEFLVGRMKVEQLTGLSG 346
Qy 347 EGRKAOEYVCELGPKIRIRVEEKVQGEKKKKAHEHPVSFSMIFNREL 392
||||| ||||| : : : ||| : : : ||||| : ||| : |||
Db 347 EGRKAOEYVCELGPKIRIRLEERAQARKESST--LKFSMIDHREV 389

RESULT 9

US-08-474-587-6
; Sequence 6, Application US/08474587
; Patent No. 5760206
; GENERAL INFORMATION:
; APPLICANT: Hltz, William D.
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Perez, Grau, Luis
; TITLE OF INVENTION: Nucleotide Sequence of
; Patent No. 5760206
; TITLE OF INVENTION: Soybean Stearoyl-ACP
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,587
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Siegel, Barbara C.
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1022-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELER: 835420
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-587-6

Query Match 69.7%; Score 1436.5; DB 1; Length 391;

Best Local Similarity 68.5%; Pred. No. 2.1e-137;

Matches 278; Conservative 44; Mismatches 53; Indels 31; Gaps 4;

Qy 1 MALKINFOCKKHHPAAFKSPPLVTRVS-----SPRVMASTVNSMSVLDNLSKSP- 51
||||| ||||| : : : ||||| : ||| ||||||| : ||| |||||
Db 1 MALRLN-----PIPTQTFSLPQMPSLRPFRRMASTLRSSGSKVEYENIKRPF 46
||||| ||||| : : : ||||| : ||| ||||||| : ||| |||||
Qy 52 -----PNIQVTHSMPPQKLEIFKSLDDMARNNVLILKSVESWQPDYLLPDPVSDGFEE 106
||||| ||||| : : : ||||| : ||| ||||||| : ||| |||||
Db 47 TPPEVHVQVTHSMPPQKLEIFKSLDDMARNNVLILKSVESWQPDYLLPDPVSDGFEE 106
||||| ||||| : : : ||||| : ||| ||||||| : ||| |||||
Qy 107 QVRELREKAKETPDYLFVVLVGDMTTEELPTYYMSMLNCDGIDKDTGAPSPAMAMWTRA 166
||||| ||||| : : : ||||| : ||| ||||||| : ||| |||||
Db 107 QVRELREKAKETPDYLFVVLVGDMTTEELPTYYMSMLNCDGIDKDTGAPSPAMAMWTRA 166
||||| ||||| : : : ||||| : ||| ||||||| : ||| |||||

Qy 167 WTAENHRGDLNKLKYLISGRVDMRKIEKTOYLIGSGMDIKSENSPYLGFIYTSFOERA 226
||||| ||||||| : : : ||||||| : ||| ||||||| : ||| |||||||
Db 167 WTAENHRGDLNKLKYLISGRVDMRKIEKTOYLIGSGMDIPTNSPYLGFIYTSFOERA 226
||||| ||||||| : : : ||||||| : ||| ||||||| : ||| |||||||
Qy 227 TETSHANTAKIAOYGDKNLAHICGSIASDEKRRHATAYTKIVERLAEIDPPTVIARADM 286
||||| ||||||| : : : ||||||| : ||| ||||||| : ||| |||||||
Db 227 TETSHANTAKIAOYGDKNLAHICGSIASDEKRRHATAYTKIVERLAEIDPPTVIARADM 286
||||| ||||||| : : : ||||||| : ||| ||||||| : ||| |||||||
Qy 287 MRKTIAMPALMYDGSSELLFKHFTAAQVRXYYSALDYCDIDLEFLVDKNVRLTGLSD 346
||||| ||||||| : : : ||||||| : ||| ||||||| : ||| |||||||
Db 287 MRKTIAMPALMYDGRDNLFDNYSVAORIGVYTAQADIDLEFLVGRMKVEQLTGLSG 346
||||| ||||||| : : : ||||||| : ||| ||||||| : ||| |||||||
Qy 347 EGRKAOEYVCELGPKIRIRVEEKVQGEKKKKAHEHPVSFSMIFNREL 392
||||| ||||| : : : ||| : : : ||||| : ||| : |||
Db 347 EGRKAOEYVCELGPKIRIRLEERAQARKESST--LKFSMIDHREV 389

RESULT 10

US-08-471-791-13
; Sequence 13, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knaut, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/762,762
; FILING DATE: 16-SEPT-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 69-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELER: 350370 CGNE

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: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 396 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-471-791-13

Query Match
Best Local Similarity 68.2%; Score 1406; DB 1; Length 396;
Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;

QY 1 MALKL---NFQCKKHHPAFAKSPLPVTRVSSPRVFMASTVNSNMYLDNLKSP----- 51
DQ 1 MALRTPVTLQSERYSFSFPPK---ANLRSPKFAMASTLGSTPKVDNAKRFQPPRE 56
QY 52 PNLQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSDGFEQVREL 111
DQ 57 VHVQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSDGFEQVREL 116
QY 112 REAKEIPDDYFVVLVGMITEALPTYMSMLNRCDGIRKETGAEPSAWMTTAWTAEE 171
DQ 117 RAKAKEIPDDYFVVLVGMITEALPTYMSMLNRCDGIRKETGAEPSAWMTTAWTAEE 176
QY 172 NRHGLLKKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFTYSFOERATFISH 231
DQ 177 NRHGLLKKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFTYSFOERATFISH 236
QY 232 ANTAKLAOHGDKNLAHICGSIASDEKRRHATATYTKIVEKLAIEDPPTVIAFADMMRKKI 291
DQ 237 GNTARNAHDKHGDVLAQICGTIASDEKRRHETATYTKIVEKLFIEDPDGTVALAFADMMRKKI 296
QY 292 TMPAHLMTDGSDELLFKHFTAVARVXYVSALDYCDILEFLVDKMNVERLTGSLDEGRKA 351
DQ 297 SMPAHLMTDGRDNLFEHPSAVAQRLGYTTAKDYADILEFLVGKMKVADLTGSLGSGRKA 356
QY 352 QEVYVCELGPRIKRVVEKVGKRRKKAHP-VSFSWTFNRELKI 394
DQ 357 QDVYVGLPRIRIRLEBRAQGRAK---EGPVVPFSWTFNDRQVKL 396

RESULT 11
US-08-926-522-2
: Sequence 2, Application US/08926522
: Patent No. 6426447
: GENERAL INFORMATION:
: APPLICANT: Vic C. Knauf
: APPLICANT: Gregory A. Thompson
: TITLE OF INVENTION: PLANT SEED OILS
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Calgene, Inc.
: STREET: 1920 Fifth Street
: CITY: Davis
: STATE: CA
: COUNTRY: USA
: ZIP: 95616
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
: OPERATING SYSTEM: Macintosh 7.1
: SOFTWARE: Microsoft Word 5.1(a)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/926,522
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/458,173
: FILING DATE: 2-June-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Elizabeth Lassen
: REGISTRATION NUMBER: 31,845
: NAME: Donna E. Scherer
```

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: REGISTRATION NUMBER: 34,719
: NAME: Carl J. Schwedler
: REGISTRATION NUMBER: 36,924
: REFERENCE/DOCKET NUMBER: CGNE DES
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (916) 753-6313
: TELEFAX: (916) 753-1510
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 396 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-926-522-2

Query Match
Best Local Similarity 68.2%; Score 1406; DB 4; Length 396;
Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;

QY 1 MALKL---NFQCKKHHPAFAKSPLPVTRVSSPRVFMASTVNSNMYLDNLKSP----- 51
DQ 1 MALRTPVTLQSERYSFSFPPK---ANLRSPKFAMASTLGSTPKVDNAKRFQPPRE 56
QY 52 PNLQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSDGFEQVREL 111
DQ 57 VHVQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVESKQPODYLPDPVSDGFEQVREL 116
QY 112 REAKEIPDDYFVVLVGMITEALPTYMSMLNRCDGIRKETGAEPSAWMTTAWTAEE 171
DQ 117 RAKAKEIPDDYFVVLVGMITEALPTYMSMLNRCDGIRKETGAEPSAWMTTAWTAEE 176
QY 172 NRHGLLKKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFTYSFOERATFISH 231
DQ 177 NRHGLLKKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFTYSFOERATFISH 236
QY 232 ANTAKLAOHGDKNLAHICGSIASDEKRRHATATYTKIVEKLAIEDPPTVIAFADMMRKKI 291
DQ 237 GNTARNAHDKHGDVLAQICGTIASDEKRRHETATYTKIVEKLFIEDPDGTVALAFADMMRKKI 296
QY 292 TMPAHLMTDGSDELLFKHFTAVARVXYVSALDYCDILEFLVDKMNVERLTGSLDEGRKA 351
DQ 297 SMPAHLMTDGRDNLFEHPSAVAQRLGYTTAKDYADILEFLVGKMKVADLTGSLGSGRKA 356
QY 352 QEVYVCELGPRIKRVVEKVGKRRKKAHP-VSFSWTFNRELKI 394
DQ 357 QDVYVGLPRIRIRLEBRAQGRAK---EGPVVPFSWTFNDRQVKL 396

RESULT 12
PCT-US91-01746-13
: Sequence 13, Application PC/TUS9101746
: GENERAL INFORMATION:
: APPLICANT: Thompson, Gregory A
: APPLICANT: Knauf, Vic C
: TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
: NUMBER OF SEQUENCES: 43
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Calgene, Inc.
: STREET: 1920 Fifth Street
: CITY: Davis
: STATE: California
: COUNTRY: USA
: ZIP: 95616
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
: OPERATING SYSTEM: Macintosh 6.0.7
: SOFTWARE: Microsoft Word 4.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US91/01746
: FILING DATE: 19910314
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherret
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-01746-13

Query Match 68.2%; Score 1406; DB 5; Length 396;
Best Local Similarity 67.1%; Pred. No. 2.7e-134;
Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;

QY 1 MALKL---NFQCKNHAFKSPPLVTVSSPRVFMASIVNSMWLDNLKSP-----51
DB 1 MALRITPVTLQSERKRSFEPKK---ANLRSKFMASTIGSTKVDNAKRFQPPRE 56
QY 52 PVLQVTHSMPPQKLEIFKSLDWMARNVLIHLKSVKSWQPDYLPDVSDFGEQVREL 111
DB 57 VHVQVTHSMPPQKLEIFKSEGMAEQNIIVHLKPYEKCWQADFLPDPASEGDEQVKEL 116
QY 112 RRRAKEIPDDYFVVLVGDMTTEALPTVMSLNRCDIGENGAESAVAMTWTAAE 171
DB 117 RARAKEIPDDYFVVLVGDMTTEALPTVQTMNTLDGVDEGTASLTPAAVMTWTAAE 176
QY 172 NRHGLDLNKLYLISGRVDMRKIEKTIQYLLISGMDIKSENSPYLGFITYTSFORATFISH 231
DB 177 NRHGLDLHTYLYLSGRVDMRQIOKTIQYLLISGMDPRTENSPYLGFITYTSFORATFVSH 236
QY 232 ANFALAQHYGCKNLAIHIGSISASDEKRAHATYTKIVEKLAELDPDTVIAEADMMRKTI 291
DB 237 GNTAHADHGHGKLAQIOGTLASDEKRHETAYTKIVEKLFELDPDGTVLAFAADMMRKTI 296
QY 292 TMPAHLMYDGSDELLEFKHFTVAORVXYVSALDYCDILEFVDMKMWVERLTGSDGGRKA 351
DB 297 SMPAHLMYDGRDNLFEHFSAVAQRLGYTTAKDYADILEFVGRMKVADLTGLSGGRKA 356
QY 352 QEYVCELGPKIRRVBEKVQGEKKKAEPH-VFSWIFENRELI 394
DB 357 QDYVCGELPPRIRLEBRAGRAK----EGPVVPFSWIFEDROYKL 396

RESULT 13
US-08-471-791-20
Sequence 20, Application US/08471791
Patent No. 5723595
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA

ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,791
FILING DATE: 6-JUNE-95
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/762,762
FILING DATE: 16-SEPT-1991
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherret
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 69-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-791-20

Query Match 67.7%; Score 1396; DB 1; Length 398;
Best Local Similarity 66.9%; Pred. No. 2.8e-133;
Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;

QY 1 MALKLNFQCK--NHPAFAKSPPLVTVSSPRVFMASIVNSMWLDNLKSP-----P 52
DB 1 MALKLNPASQPPNPFSS-ARPISTFRSPKFLCLASSSSALSKVEVSLKKPTTPKEV 59
QY 53 NLQVTHSMPPQKLEIFKSLDWMARNVLIHLKSVKSWQPDYLPDVSDFGEQVREL 112
DB 60 HVGVLHSMPPQKLEIFKSEGMAEQNIIVHLKPYEKCWQADFLPDPASEGDEQVREL 119
QY 113 ERAKKEIPDDYFVVLVGDMTTEALPTVMSLNRCDIGKDTGAPSPKAMMTWTAAEEN 172
DB 120 ERAKKEIPDDYFVVLVGDMTTEALPTVQTMNTLDGVDEGTASPTSWAWTWTAAEEN 179
QY 173 RHBDLNLNKLYLISGRVDMRKIEKTIQYLLISGMDIKSENSPYLGFITYTSFORATFISHA 232
DB 180 RHBDLNLNKLYLISGRVDMRKIEKTIQYLLISGMDPRTENSPYLGFITYTSFORATFISHG 239
QY 233 NTAKLAQHYGCKNLAIHIGSISASDEKRAHATYTKIVEKLAELDPDTVIAEADMMRKTI 292
DB 240 NTAQAQKEHODLKAQIOGTLADEKRHETAYTKIVEKLFELDPDGTVMAFADMMRKTI 299
QY 293 MPAHLMYDGSDELLEFKHFTVAORVXYVSALDYCDILEFVDMKMWVERLTGSDGGRKAQ 352

```

0Y 223 NFAKLAOHYQKGNLHAGCGSTASDEKRIATATYKIVKLAELIDPTTYIAADMMRRKIT 292
      |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 NTAQAKAEHGDJLKAQICGTIAADEKRHEHTATYKIVKLFELIDPGTYMAFADMMRRKIS 299
      |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
0Y 293 MPAHLMYGSDELFEKHTTAQAVARXYVSALDYCDILEFLVDKNVVERTJGSDGGRKAQ 352
      |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 MPAHLMYGRDESLFDNFTSSVAQRLGYVTIANDYDILEFLYGRKRIESTJGSGGNKAQ 359
      |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
0Y 353 EYVCELGRIIRVEERVOGKEKKKKAHEHPVSFTIENBELI 394
      |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 360 EYICGLTPRIRRLDERAQAQAKGP---KVPFSWIHDREVQI 398
      |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
PCT-US91-01746-20
; Sequence 20, Application PC/US9101746
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knaut, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 Inch, 1.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 19910314
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-1510
; TELEFAX: (916) 753-6313
; TELE: 350370 CGNE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 398 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-01746-20

Query Match 67.7%; Score 1396; DB 5; Length 398;
Best Local Similarity 66.9%; Pred. No. 2.8e-133;
Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;

0Y 1 MALKINPQCKR--NHRAFAKSPLEVTYVSSPRVPMASGVNSMAYLNTKSP-----P 52
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MALKINPLASQYINPSS-ARPPISTFRSPKFLCLASSSPALSKVEVSLKKPPTPPREV 59
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
0Y 53 NLOVTHSNPQKLETFKSLDDMARNNVLIHLKSVKSWQPODYLDPDVSDFEEDQVREL 112
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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```

Db      60  HVQVLSMPPOKIEIFKSMEDWAEQNLTLQKOVEKSWQPODFLPDPASDGEFEDQVRELR 119
Qy      113  ERAKEIPDDYFVVLVGDMMITEFALPTYMSMLNRCDG IKDETGAEPSSAMAMTRAMTAEN 172
      120  ERARELPDDYFVVLVGDMMITEFALPTYQTMINTLDGVREDETGAESPMAITWTRAMTAEN 179
Qy      173  RHGDLINKYLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFITYTSFOERATFISHA 232
      180  RHGDLINKYLYLSGRVDMRKIEKTIQYLLIGSGMDPRTENNPPYLGFIYTSFOERATFISHG 239
Qy      233  NTAQKLAQHGDKNLAHIGSISASDEKRHATAYTKIVEKLAIEDPDTVIAFADMMRKKIT 292
      240  NTAQKKEHGDCLKAQICGTIADEKRHETAYTKIVEKLEFIDPDGTYMAFADMMRKKIS 299
Qy      293  MPAHLMYDGSDELLFKHFTAVAOQVXYVSALDYCDILLEFLVDRKWNVERLTGLSDEGRKAQ 352
      300  MPAHLMYDGRDESLFNFSSVAQRLGVYTAQDYADILLEFLVGRWKIESLTGLSGEGNKAQ 359
Qy      353  EYVCELGPKIRVREEKVQGEKKKKAHHPVSFSMIFNRELKI 394
      360  EYLCGLTPRIRLDERAQARAKGP--KVPFSMIDHREVOL 398

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Search completed: December 1, 2002, 21:22:08
 Job time : 20 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 21:12:16 ; Search time 2407 Seconds
(Without alignments)
9043.097 Million cell updates/sec

Title: US-09-732-597-1
Perfect score: 1344
Sequence: 1 caaccacagaataaataa.....tttgagtttaagtaaaaa 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estbda:*
2: em_estbhum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estloy:*
6: em_estlpl:*
7: em_estlro:*
8: em_estlhc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_estl3:*
12: gb_estl4:*
13: gb_estl5:*
14: gb_estl6:*
15: em_estfun:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	513	38.2	1780	11	AY104235 Zea mays
2	491.2	36.5	1623	11	AY104301 Zea mays
3	424.4	31.6	702	13	BM436665 VVA008A04
4	382.6	28.5	708	13	BI271942 NF016F09F
5	372.2	27.7	712	12	BG269539 LO-3624T3
6	368.8	27.4	699	14	B0027980 QHG9D05.Y

7	368.6	27.4	804	10	BE559272 HV_CEB002
8	360	26.8	641	10	AV933496 AV933496
9	358.8	26.7	811	10	BE643410 Cr12_8_L12
10	355	26.4	628	10	AW509087 s139h08.Y
11	353.4	26.3	852	14	B0510820 EST618235
12	351	26.1	1055	12	BG837910 Zml0_10c0
13	343.2	25.5	671	10	AV914373 AV914373
14	341.8	25.4	612	9	AT1730379 BMLG1676
15	341.6	25.4	606	10	BE610498 sq77b04.Y
16	340.8	25.4	634	14	B0149496 NF105B07F
17	340.6	25.3	619	13	BM323364 PIC1_18.D
18	339.8	25.3	593	13	BI425553 saf32910.
19	338.8	25.2	793	12	BG888941 EST514792
20	332.8	24.8	596	10	AV934363 AV934363
21	331	24.6	633	13	BI179928 EST520873
22	321.4	23.9	793	12	BG887868 EST513719
23	321.2	23.9	636	10	AW395273 sh46a10.Y
24	321.2	23.9	662	9	AJ432511 AJ432511
25	319.4	23.8	621	13	BJ464232 BJ464232
26	318.4	23.7	655	10	AW066113 687006D02
27	317.6	23.6	569	13	BM322551 PIC1_6_C0
28	314.2	23.4	566	13	BI468759 sa103a07.
29	313.8	23.3	971	12	BG446852 GA_Eb003
30	310	23.1	556	13	BI674398 sah71907.
31	309.8	23.1	752	13	BI933357 EST533246
32	305.2	22.7	763	13	BI934897 EST554786
33	304.6	22.7	650	10	BE427627 PSR7275.I
34	302.8	22.5	885	12	BF268770 GA_Eb000
35	302.4	22.5	604	13	BJ481070 BJ481070
36	302	22.5	857	12	BF271279 GA_Eb001
37	301.8	22.5	714	12	BG889927 EST515778
38	300.4	22.4	622	10	BE517215 WHE0615_C
39	299.4	22.3	708	14	BQ802244 WHE2823_G
40	296.4	22.1	736	13	BJ247775 BJ247775
41	295.2	22.0	700	12	BG596559 EST495237
42	294.2	21.9	561	10	AW030327 EST723582
43	294	21.9	745	14	BQ112398 EST597974
44	291.2	21.7	576	12	BG352880 sab92e03.
45	291	21.7	745	13	BJ167132 BJ167132

ALIGNMENTS

RESULT 1	AY104235	1780 bp	mRNA	linear	HTC 25-MAY-2002
LOCUS	AY104235	PCO105183	mRNA sequence.		
DEFINITION	Zea mays				
ACCESSION	AY104235				
VERSION	AY104235.1	GI:21207313			
KEYWORDS	HTC.				
SOURCE	Zea mays.				
ORGANISM	Zea mays.				
REFERENCE	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hainey,M., Morgante,M. and Tingey,S.V.,				
AUTHORS	Maize Mapping Project/DuPont Consensus Sequences for Design of				
TITLE	Overgo Probes				
JOURNAL	Unpublished (2002)				
REFERENCE	2 (bases 1 to 1780)				
AUTHORS	Coe,E.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of				
FEATURES	Missouri, Columbia, MO 65211, USA				
source	1. 1780				
	/organism="Zea mays"				
	/db_xref="MaizeDB:636088"				
	/db_xref="taxon:4577"				
	/clone="PCO105183"				

/clone_lib="Maize Mapping Project/DuPont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of Bacs in conjunction with the Maize Mapping Project"

BASE COUNT 420 a 454 c 494 g 412 t
ORIGIN

Query Match 38.2%; Score 513; DB 11; Length 1780;

Best Local Similarity 70.2%; Pred. No. 2.4e-97;
Matches 687; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

```
QY 192 AAGTCCGCAATCTTCAAGTACATCTCTATGCCACCCCAAAAGCTTAAATATTCAA 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 409 AAGGAGGACATGTCACAGTTACATTCATGCCACCTCACAGATGAAATTTTCAA 468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 252 GTCCCTGATGATTTGGCTAGGACAAATGTTGATTCACCTCAAAATCTGCGAGAATC 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 469 GTCCCTGATGATTTGGCTAGGACAAATGTTGATTCACCTCAAAATCTGCGAGAATC 528
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 312 TTGGCAACCAAGACTACTTCCGCGATCCGCTGACAGCGATTTGAGAGCAAGTCCG 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 529 TTGGCAACCAAGACTACTTCCGCGATCCGCGATCCGCTGACAGCGATTTGAGAGCA 588
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 372 CGAGTTGAGGGAAGGCGCAAGAGATTCGCGACGACTATTTTGTGGTGTGGTGGAGA 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 589 CGAGTTGAGGGAAGGCGCAAGAGATTCGCGACGACTATTTTGTGGTGTGGTGGAGA 648
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 432 TATGATCACAAGAGAGCACTTCCAAATATATGTTCTATGCTCAATATAGTGTGATAT 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 649 CATGATTCACGAGAGAGCTTACCAATATACAGACTATGCTTAAACACCCCTGACGCGT 708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 492 TAAGATGAGACTGGGCTGAGCCCAAGTCTTGGGCAATGTGAGACTAGGCACTGAC 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 709 CAGAGATAGAGAGGTGCAAGGCCCACTGCGGCTGTTTGAACGAGGCACTGAC 768
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 552 CGAAGAGATATGACATGTTGACCTTCTCAATAGTACCTTTTATTTGTGGAAGGGTTGA 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 769 TGAGAGAGAGAGAGCTGTTGATCTGCTCAACAAGTATATGTAAGTCTGAGAGGGTGA 828
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 612 TATGAGAGAAATTTGAGAGAGACTATTCATATCTCATCGGCTCAGGAATGATATCAAGTC 671
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 829 TATGAGAGAGATTTGAGAGAGACTATTCATATCTCATCGGCTCAGGAATGATATCAAGTC 888
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 672 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 889 TGAGATATATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 948
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QY 732 ATCCATATCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 791
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Db 949 CTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1008
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 792 CTGGGGCTCATCGCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1009 CTGGGGCTCATCGCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1068
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QY 852 AAGAGTGCCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1069 AAGAGTGCCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1128
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QY 912 AAAAATTAACAATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 971
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Db 1129 GAAGATTCATATGCTGCGCCACCTCATATGTTACGCGGAGAGAGAGAGAGAGAGAGAGAGAG 1188
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QY 972 TTTCACGGCGGTTGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031
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Db 1189 CTTCATTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1248
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Db 1249 CGAGTTCTCTGTCAGACAGTGGAGAGGCGAGACTGCTGCTGCGGTGAGAGGAA 1308
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Db 1309 CAAGGCGGAGAGACTTCTGTTGACACCTTGTCTTCAAGATACAGAGAGCTGGAGAGAGAGG 1368
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QY 1152 GCAGGGAGAGAGAGAGAA 1169
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```

RESULT 2

AY104301 1623 bp mRNA linear HTC 25-MAY-2002

LOCUS Zea mays PC0071296 mRNA sequence.

DEFINITION Zea mays PC0071296 mRNA sequence.

ACCESSION AY104301

VERSION AY104301.1 GI:21207379

KEYWORDS HTC.

SOURCE Zea mays.

ORGANISM Zea mays.

REFERENCE 1 (bases 1 to 1623)

AUTHORS Halney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,

Arthur, L.W., Hanafey, M., Morgan, M., and Tingey, S.V.

Maize Mapping Project/DuPont Consensus Sequences for Design of

Overgo Probes

Unpublished (2002)

2 (bases 1 to 1623)

CoE, E.C.

Direct Submission

Submitted (25-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, MO 65211, USA

Location/Qualifiers

1..1623

/organism="Zea mays"

/db_xref="MaizeDB:633889"

/db_xref="taxon:4577"

/clone="PC0071296"

/clone_lib="Maize Mapping Project/DuPont Consensus

Library"

/note="this sequence is part of a project of EST

assemblies resulting from the application of public

contigs to seed DuPont contigs; this resource was

assembled by DuPont as part of a collaboration for the

overgo addressing of Bacs in conjunction with the Maize

Mapping Project"

BASE COUNT 441 a 376 c 445 g 361 t

ORIGIN

Query Match 36.5%; Score 491.2; DB 11; Length 1623;

Best Local Similarity 67.4%; Pred. No. 9e-93;

Matches 710; Conservative 0; Mismatches 334; Indels 9; Gaps 1;

QY 201 AAATCTCAAGTCACTCTATGCGACCCCAAAAGTGAATAATTCAGTCCCTTGA 260

Db 258 ACATGCCCAATATACCATCTACACACCTCAAAAGCGGAGATTTTCATTCACCTCA 317

QY 261 TGAATGGGCTAGGAGAAATGTGATTCACCTCAATCTGTGAGAGAAATCTGGCAACC 320

Db 318 ACCTTGGGCGCAAGATTAACCTGTAACCTGTAAGCCGTTGAAAGATCATGGCAGCC 377

QY 321 ACAAGACTCTCTGCGGATCCGCTGTCAGAGAGATTCGAGAGCAAGTGGCGGATGAG 380

Db 378 ACAGGACTCTCTACAGAGCTCTCTCTGATGGGTTTATGATGAGATTAAGCAACTGAG 437

QY 381 GGAAGAGCGCAAGAGATTCGCGAGCACTATTTTGTGTTTGTGATTTGAGATATGATCAG 440

Db 438 GGAAGAGCGCAAGATTAAGATTAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 497

QY 441 AGAAGAGAGCACTTCCAAATATATGTTCTCAATAGTGTGATGATGATGATGATGATGATGATG 500

Db 498 TGAGAGACCTTACCTACATACCAACAATGCTTACACTCTTGATGGAGTCCGGATCA 557
Qy 501 GACTGGGGCTGAGCCAGCTGCTTGGGCAATGTGACTAGGCGATGAGTCCGGAAGAGA 560
Db 558 AACTGGTCAAGTCCAACACAGCGGCTTGGACAAAGGCGATGAGACGTGAAGAGAA 617
Qy 561 TAGACATGTGACCTTCTCAATTAATGACTTATTTGCTGGAAGGTTGATATGAGAA 620
Db 618 CAGACATGCTGCTTCACTTAACAACTACATGACCTTACTGAGCGGTTGACATGAACA 677
Qy 621 AATTGAGAAAGCTATTCATATCTCATGCGCTCAGGAATGATATCAAGTGAAGAAAG 680
Db 678 AATTGAGAAAGCACTACATATCTCATGCTTCCGGAATGATCTCGAGACTGAGAACAA 737
Qy 681 CCCCTACCTAGGCTTCATCTACATCTCTCCAGAGAGACACCTTCATATCCCATCC 740
Db 738 CCCCTACTGGTTCCTCTACATCATTTCCAGAAAGGCGCAACATTTGTGCGCATGG 797
Qy 741 CACACACACCAAGCTGGGCCAACATAGGCGACAAAGAACTGCTCACATCTGGCGCTC 800
Db 798 GAATTACTCAAGGCAATGCGCAAGAGATATGCTATCTCAAGCTGGGCCACATATGTGGCAC 857
Qy 801 CATGCTCTCCGAGAGAGCGCCACAGCTTACACAGATGCTGGAAGAGCTCGC 860
Db 858 GATGACACCGCATGTGAAGCGCCAGAAACAGCTTACACAGATATGTGAGAGAGCTTT 917
Qy 861 TGAGATGACCCCGACACACAGATATTTGCTTTCAGATATGATGCGCAAAATAATAC 920
Db 918 CGAGATGACCCCTGATTTACAGAGTGTGCTTGTCTGACATGATGAGCAAGATAC 977
Qy 921 AATGCGACGCACTTGTATGTAGCGAGAGATGAGCACTCTTTTAAACATTTACGCGC 980
Db 978 GATGCGACCCCATCTCATGTATGAGCGATGAGCAACCACTGTTGACACTTACGCGC 1037
Qy 981 GATTCTCAGAGAGAGTGGGCTTATTTCTGCTTGTGATTTATGCGACATTTGAGATTTCT 1040
Db 1038 GTGCGCGAGAGGCTGGGCGCTTACACCGCCAAAGACTACCGGACATCTTGAGTTCT 1097
Qy 1041 GGTGATTAATGGAATGTGGAAGAGCTTACAGGCGCTGTGCGAGAGGCGCAAAAGCGCA 1100
Db 1098 GTTCAGAGGTGGAAGAGTGGCGAGCTCACAGGCGCTGTGTGAGAAAGGAGAGCGCGCA 1157
Qy 1101 GGAATATGTGTGTAATTTGGTCCCAAGATTAGGCGAGTGGAGAGAAAGTCCAGGGGAA 1160
Db 1158 GGACTTGTCTGTACTCTTGGCGCCAGAGATCAGGCGCTGATGATGAGCTCAACCGCAG 1217
Qy 1161 GAGAGAAAGAAAGAAAGCTGAGACCTCTGTTCTTTCAGCTGATTTTCAATCGGAGTT 1220
Db 1218 GGGCAGACA-----AGCACCGGTTATTTCTTTCACTTGGGTTTATGACCGCAGGT 1268
Qy 1221 GAAGATATGAACAGAGAGGAAAGGAAATGAGAG 1253
Db 1269 GCAGCTTAATCAAGACGCTAGGCAATGTGGG 1301

RESULT 3
LOCUS BM436665
DEFINITION VVA008A04.52913 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay
ACCESSION BM436665
VERSION BM436665.1 GI:18458387
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 702)
AUTHORS Cramer, G.R. and Cushman, J.C.
TITLE An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay

JOURNAL Unpublished (2002)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 008 row: A column: 04
Seq primer: T3 20mer
High quality sequence stop: 702.
Location/Qualifiers
1..702
/organism="Vitis vinifera"
/db_xref="taxon:29760"
/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/issue_type="leaf"
/dev_stage="juvenile and adult"
/note="vector: Lambda Uni-zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda Uni-zapXR vector and cDNA synthesis kit."
BASE COUNT 210 a 144 c 176 g 172 t
ORIGIN
Query Match 31.6%; Score 424.4; DB 13; Length 702;
Best Local Similarity 75.5%; Pred. No. 9.1e-79;
Matches 527; Conservative 0; Mismatches 171; Indels 0; Gaps 0;
Qy 259 GATGATGGGCTGGAACAATGTGTGATTCACCTCAATCTGCAGAAATCTGGCAA 318
Db 2 GAAATTTGGGCTGAGAGAACTTTTGTTCCTGAGCGAGTGAATCTGGCAA 61
Qy 319 CCACAAGACTACTTGGCGGATCCGGTGTGACAGAGATTCGAGAGCAAGTGGGAGTTG 378
Db 62 CCACAGATTTTGTACAGATCTCGTGTGTGATGATTCATGACAAAGTCAAGAACTA 121
Qy 379 AGGGAAGGGCCCAAGAGATTTCCGACGACTATTTGTGTGTTAGTTGAGATATGATC 428
Db 122 AGGGAAGGGCCCAAGAGAGCTTCAGATGATTTGTTGTTGGTGGAGATATGATC 181
Qy 439 ACAGAAAGACATCTCAACATATATGTATGCTCAATAGGCTGATGATTAAGAT 498
Db 182 ACTGAAGAGCCCTTCCAACTTACCAAAACATGCTTAATCTTGGAGGGTTGGGAT 241
Qy 499 GAGACTGGGCTGAGCCAGTGTGGCAATGTGACTAGGCGATGAGTGGCGAGAG 558
Db 242 GAACAGAGTGCAGGCTCACCCTCTTGCGCAATTTGGACAAGGCGATGAGTGCAGAGAG 301
Qy 559 AATGACATGCTGACCTTCTCAATTAAGTACCTTTATTTGTCTGGAAGGTTGATAGG 618
Db 302 AACGAGCATGTGACCTTCTCAACAAGTACTATATCTGTGAGAGAGTACATAGAG 361
Qy 619 AAATTTGAGAAAGCTATTCATATCTCATGCGCTCAGAGATGATATCAAGTACAGAAAC 678
Db 362 CAATTTGAGAAAGCAATTCATATTTGATGATGATGAGATGATGATGATGATGATGAT 421
Qy 679 AGCCCTACCTAGGCTTCATCTACATCTCTTCCAGAGAGAGAGCAACTTCATATCCAT 738
Db 422 AGTCCCTACTCGGGTTTCATCTACCTTCTTCCAGAAAGGCGCATTCCTCCAT 481
Qy 739 GCCACACACCAAGTGGGCCAACACATPACGCGAGCAAACTCGCTCATCTGCGGC 798
Db 482 GGCACACACTGCCAGGATGCCAAGAGCATGGGATATGAAGTTGGCTCAATATATGTGT 541
Qy 799 TCCATGCTCTCGACAGAAAGGCGCACAGCTCAGACCAAGATCTGTGAAAAGCTC 838
Db 542 ACAATTTGCTCAAGATGAGAGCGGCATGAAACTGCTACACCAAGATATGTGAAAAGCTC 601

QY	859	GCTGGATGACCCCCGACACACAGTAATGCTTTGGCAGATATGATGCGCCAAATAAATA	918
Db	602	TTTTGATTTGATCTCGATGGAAGTACTGCTTGGCTGACATGATGAGAGAAATTC	661
QY	919	ACAAATCCAGCCACTTGATGTATGACGAGAAATGACGA	956
Db	662	TCATGCGCTGCTACACTGATGATGATGCGCCGTGATGA	699
RESULT 4			
LOCUS	Bi271942		
DEFINITION	NP016FP09FL1P078 Developing flower Medicago truncatula cDNA clone		
ACCESSION	Bi271942		
VERSION	Bi271942.1		
KEYWORDS	EST.		
SOURCE	barrel medic.		
ORGANISM	Medicago truncatula		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.		
REFERENCE	1 (bases 1 to 708)		
AUTHORS	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.		
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: May GD Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380 Email: gdmay@noble.org Insert length: 708 Std Error: 0.00 Plate: 016 row: F column: 09 Seq primer: TCACACAGGAACACGCTATGAC. Location/Qualifiers		
FEATURES			
Source	1..708		
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	/clone="NF016F09FL"		
	/clone_lib="Developing flower"		
	/tissue_type="Developing flowers"		
	/deriv_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods."		
	/note="Vector: Lambda zap; cDNA was prepared from polyA+ RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-zap XR vector (Stratagene) and packaged using the GigaPack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-zap XR vector using EXASist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."		
BASE COUNT	194 a 137 c 181 g 190 t		6 others
ORIGIN			
Query Match	28.5%;	Score 382.6;	DB 13; Length 708;
Best Local Similarity	71.0%;	Pred. No. 5.1e-70;	
Matches 502; Conservative 0;	Mismatches 205;	Indels 0;	Gaps 0;
QY	406	GACATTTTGGGCGTGTAGTTGAGATATGACAGAGAAGACGACTTCCACATATATG	465
Db	1	GATTACTTTGTTGTTCTGCTGAGATATGGTCACAGAAAGCTCTTCTACTTACCA	60
QY	466	TCATGCTCAATAGGTGATGATGATTAAGATGAGACTGGGCGTAGCCCCAGTGCCTGG	525

Db	ACTATGCTTAATACCTTTGGACGGAGGTCTGTATGAACACAGGTGCCACGCCCTACTCCCTTG	120
QY	526 GCATGTGTGAGCTAGGGCAGTATGACATGCCGAGAGAAATGACATGTGACCTTCTCAATTAAG	585
Db	121 GCTATTGTGACAAAGACATGAGACAGCTGAAGAAAATAGACACGGTGATCTCTTAAACAAG	180
QY	586 TACCTTTATTTGTCGGAAGGGTGTATGAGAGAAAATTGACAAAGACTTTGCAATATCTC	645
Db	181 TATCTTTACTTTCGCGGCGCTGTATGACACAATTTGAAAGACAATTCAGTACTTG	240
QY	646 ATGCGCTCAGAAATGATATTCAGATCAGAAAACAGCCCTACCTAGGCTTCATCTACACA	705
Db	241 ATTGGCTGTGAAATGGATCTCTGAGCTGGAAPVAGCCCTTACTTGGCTTATTCAGACT	300
QY	706 TCTCTTCAAGACAGACAACTTCATATCCCATGCCACACAGCCAAGCTGGCCACAC	765
Db	301 TCATTTCAAGACAGGCAACCTTTATATCGACATGGAAACACAGCTAAGCTTCTAAGAA	360
QY	766 TACGGGACAAAGACCTGCTCAGATCTGCGGCTCCATCGCCGACAGAGGCGCC	825
Db	361 CGCGCGATTTTAAAGTTGGCTCAGATCTGTGGTCTGATTTGCCATGATGAGAAAGCCAT	420
QY	826 GCCACAGCTTACACCAAGATCTGGAAGAAAGCTGCTGAGATGACCCGACACAACAGTA	885
Db	421 GAGACTGCTTACACAAGATAGTGGAAAGCTATTGGAGATGATTCGTATGGAACAGTT	480
QY	886 ATTGCTTTTGGCAGATATGATGGCGAAAAAATAACAAATCCAGCCGACTGATGATGACAC	945
Db	481 ATTGCTTTTGGCAGATATGATGAGAAAGAAATTTGCTATTCACAGCAACCTGATGATGAT	540
QY	946 GGAAGTGAAGAACTCTTTTAAACATTTTCAAGCGGCTGTCTCAGAGATGAGGGTTTAT	1005
Db	541 GCGCGAGACAGCAATCTGTTGATTAACATATCTGCTGTGGCCAGCGCATTTGAGATCTAC	600
QY	1006 TCTGCGTTGAGATTTATTTGGACATCTTTAGAGTTTCTGTTGATGATTAATGCAATGCAAAAG	1065
Db	601 ACTGCTCAAGAGCTATGCTGATATTAATCTGTTCTGTTGCTGGAGGAGAAAGGGGNCGAC	660
QY	1066 CTTACGGGGCTGTGCGAGAGGGGGAAGGCGAGAAATATGTGTG	1112
Db	661 ATTAACCGGACTTTCAGGTGANGACNAAGACAGAGATATGTTTG	707
RESULT 5		
BG269539	712 bp	linear
LOCUS	L0-3624T3 Ice plant Lambda Uni-Zap XR expression library, 0 hours	
DEFINITION	Nacl treatment Mesembryanthemum crystallinum cDNA clone L0-3624 5',	
ACCESSION	mRNA sequence.	
VERSION	BG269539	
KEYWORDS	BG269539.1 GI:12975736	
SOURCE	EST.	
ORGANISM	common iceplant.	
	Mesembryanthemum crystallinum	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
	Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.	
REFERENCE	Cushman, J.C.	
AUTHORS	An expressed sequence tag database for the common ice plant,	
TITLE	Mesembryanthemum crystallinum	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Cushman JC	
	Department of Biochemistry	
	University of Nevada	
	MS200, Reno, NV 89557-0014, USA	
	Tel: 775-784-1918	
	Fax: 775-784-1650	
	Email: jcushman@unr.edu	
	PCR Primers	
	FORWARD: T7	
	BACKWARD: T3	

QY	513	GGCCGATGGTGGGCAATGGACTGGGCGATGGATGGCGAAGAGAAATAGACATGGTGA	572
Db	246	CCCTACTCTTGGGCGATATGGGACTTGGGCGTTGGACCGCTGAAGAAACAGCGACGGTGA	305
QY	573	CCCTTCATTAAGTACCTTTAATTTGTCGGAAGGGTTGATATGAGGAAAAATTGGAAGAC	632
Db	306	TCTTCTACATCAGTATCTGTATCTTATGCGGGGGGGTGCAGATGAGGACATTCAGAAAGAC	365
QY	633	TATTCATATTCATACGCGGTGCAAGGATGATATCAGTCAGTGAAGAAACAGCCCTTACTAGG	692
Db	366	AATTGAGTACCTCATTTGGGTTCTGGATTGGACCCCGGACGAAACAGTCTTACCTTGG	425
QY	693	CTTCATCTACACATCCCTTCCAGAGAGCAACCTTCATATCCCATGCCACACACACCAA	752
Db	426	GTTCTATCTACACTTCATTATTTCAAGAGGGTGCACCTTCATCTCAGCAAGAAACACACACCG	485
QY	753	GCTGGCCCAACACTACGCGGACACAGAACCTCGCTCAGATCTGGGGCTCATCGCCCTCGA	812
Db	486	GCACCCAAAGGAGCATGGTGGACGTAGAGCTGACTCAAAATGTGGGATTAATTGCACTTGA	545
QY	813	CGAGACGCGCCACGCGACAGCCTPACACCAAGATCGGGAAGAGCCTGCGATGTCGACCC	872
Db	546	TGAAGAGGAGGACGAACCGCCTAACACAAAATAGTAAAAACTTTTGAATTTGACCC	605
QY	873	CGACACAACAGTAAATGTCTTTTGGCAGATATGATGGCAAAAAAATPACATGCGACGCGA	932
Db	606	GGACGCGCACTGTTCCGCTTTTGTGCATGATGATGAGGAAAGAGATCCTCATGCGCTGCACA	665
QY	933	CTTGATGTACGCGAGAGTGAAGCACTCTTTT	965
Db	666	CTTGATGTACGAGTGGGCGTGAGCATTAACCTCTT	698

RESULT 7
 BE559272
 LOCUS
 DEFINITION
 BE559272 804 bp mRNA linear EST 23-OCT-2001
 HV_CEB0022EF16f Hordeum vulgare seedling green leaf EST library
 HVCDDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
 HV_CEB0023EF16f, mRNA sequence.
 BE559272
 ACCESSION
 VERSION
 BE559272.2 GI:13266511
 KEYWORDS
 EST.
 SOURCE
 Hordeum vulgare.
 ORGANISM
 Hordeum vulgare.
 Hordeum vulgare.
 Embryotax; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 ; Triticeae; Hordeum.
 1 (bases 1 to 804)
 REFERENCE
 Wang,R., Close,T.J., Kleinholz,A., Wise,R., Wei,F., Begum,D.,
 Fritsch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
 D.W., Penton,R.D., Oates,R. and Main,D.
 Development of a genetically and physically anchored EST resource
 for barley genomes: Blumeria infected incompatible (Mla6) seedling
 leaf cDNA library
 JOURNAL
 COMMENT
 Unpublished (2001)
 On Aug 14, 2000 this sequence version replaced gi:9823678.

FEATURES
source

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location/Qualifiers
1..804
/organism="Hordium vulgare"
/cultivar="C116151 (MLab)"
/db_xref="taxon:513"
/clone="HV_CEB0033F16f"
/clone_lib="Hordium vulgare seedling green leaf EST
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library HVCdNA0005 (Blumeria challenge)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note=Vector: LambdaZAP; Site_1: EcoRI; Site_2: XhoI;
C.I. 16151 (Mia6) plants were greenhouse grown in the R
wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874 (AvrMia6
of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wei, Wise). In the TJ Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give pBluescript SK(-) cDNA
phagemids (Choi, Close). Phagemids were plated and picked
at the Clemson University Genomics Institute (CUGI) (Begum
Palmer, Fritsch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates
Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
<http://www.genome.clemson.edu/projects/Barley>. To order
this clone see <http://www.genome.clemson.edu/orders> Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

Query Match	Best Local Similarity	Score	DB	Length
27.4%	68.8%	368.6	10	804
Matches	Conservative	0	Mismatches	229
			Indels	0
			Gaps	0

QY	743	ACACAGCCACACTGGCCCCACACACTAGCGCGCAAGAACCTCGCTCACATCTGCGGCGTCCA	802
Db	610	ATACCGCTTAGCGATGCGACAGCAATTTGGGGACCTTTAACTGGCCCAAGATATGTGGCACAA	669
QY	803	TGCGCTCCGACGAGAAAGCGCCACGCGCACACTACACCAAGATCGTGGAAAAAGTTCGCTG	862
Db	670	TAAACGCTGATGAGAAAGCGCCATGAAGCGCTTACACCAATATAGTAGAGAGCTTTT	729
QY	863	AGATGACCCCGACACAAACAGTAATTGCTTTTGCAGATATGATGCGCAAAAAATACAA	922
Db	730	GAATTAATCTGACACTACACGGGGGCTTGCTTTGCTGACATGATGAAGAAAGAAACTCAA	789
QY	923	TGCGAGCGCACTGA	937
Db	790	GCGCTGCTCATCTTA	804
RESULT	8		
AV933496			
LOCUS			
DEFINITION	AV933496	641 bp	mRNA linear EST 18-JAN-2002
ACCESSION	AV933496		
VERSION	AV933496.1	GI:18229293	
KEYWORDS	EST.		
SOURCE	Hordeum vulgare subsp. vulgare.		
ORGANISM	Hordeum vulgare subsp. vulgare		
REFERENCE	1 (bases 1 to 641)		
AUTHORS	Sato, K., Saisho, D. and Takeda, K.		
TITLE	Baleo EST sequencing project in NIG and Okayama Univ		
JOURNAL	unpublished (2002)		
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp.		
FEATURES			
source	1..641		
	/organism="Hordeum vulgare subsp. vulgare"		
	/cultivar="Haruna Nijo"		
	/db_xref="taxon:112509"		
	/clone="baal7c22"		
	/clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"		
	/tissue_type="top three leaves"		
	/dev_stage="adult, heading stage"		
BASE COUNT	168 a 146 c 165 g 162 t		
ORIGIN			
Query Match	26.8%	Score 360:	DB 10: Length 641:
Best Local Similarity	73.6%	Pred. M. 2.8e-65:	
Matches 459:	Conservative 0:	Mismatches 165:	Indels 0: Gaps 0:
QY	252	GTCCCTGATGATGGCGTAGAACAAATGTCTTATCACCCTCAAAATCTGTCGAGAAATC	311
Db	13	GTCCTTATGTTGGTGGCTAGAGTAATCTGTGCTGTGATCTTAAGCCAGATGACAAAGT	72
QY	312	TTTGCAACCAAGACTTCTTCCGATCCGCTGTGACAGCGATTCGAGAGCAAGTCCG	371
Db	73	TTGGCAGCCACAGGATTTCTCCCTGATCCAGCAATCATGATGATTTCAAGTGAAGTTAA	132
QY	372	GGAGTTGAGGGAAGGCGCAAGAGATTCGCCGAGACATTTTGGTGGATTTGGGAGAGA	431
Db	133	GGAATCTGACAGACACTGCCAAGAAATTCCTGATGATTAATCTTGTGTTGGTGGAGA	192
QY	432	TATGATTCACAGAAAGCACTTCCAAATATATGCTATGCTCAATAGTGTGATGTAT	491

DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	193	CATGATTACCGAGGAGAGCTCTTCTTACACTACACAGACTATGCTTAACACCCTCGANTGGT	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
QY	492	TAAAGATGAGACATGGGGCTGAGGCCAGTGCTTGGGCAATGTGACTAGGCACTGC	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
Db	253	CCGAGATGAAACAGGTGCTAGGCCACTGCTGGGCTTTGGACGAGGCGATGAGCTGC	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
QY	552	CGAAGAGAAATGACATGSGTGAACCTTCCAAATPAGTACCTTATTTGTCGTGAAAGGTTGA	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
Db	313	TGAGAGAGATAGGCGTGGTGTGACCTCTTAACCAAGATATCTGATCCACTGTGGAGAGTGA	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
QY	612	TATGAGGAAAAATTGAGAGACTATTCATATCTCATCGCTCAGGAATGATATCAATGC	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
Db	373	CATGAGGCAAAATGTGAAGACATTCATATCTTATTTGGCTGTGGAATGGACCATGAGAC	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
QY	672	AGAAAACAGCCCTTACCTAGGCTTCATCTACACATCTCTCCAAAGAGAGACACCTTCAT	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
Db	433	AGAGAACATATCCATATCTTGGCTTCATCTACACCTCTCTCCAAAGAGCGCTGGACCTTCAT	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
QY	732	ATCCCATGCGCAACAGCGCAAGCTGCGCCCAACACTAGGCGGCAACAGAACCTTCGCACAT	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
Db	493	CTCACATGAGAAACACTGCTCGCCATGCCAAGAGACTTGGTGAACCTTGGACACAT	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
QY	792	CTGCGCTTCACATGCGCTCCGACGAGAACGCGCACGCCACAGCTCACCAAGATGTTGA	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
Db	553	CTGTGGCATTCATCGCTCTGGATGAGAAAGCGCATGAGACTGCATACACCAAGATGTTGA	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
QY	852	AAAGCTCGCTGAGATGAGACCCCGA	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
Db	613	GAAAGCTGTTGAGATTGATCTCGA	BE643410	811 bp	mRNA	linear	EST 01-SEP-2000					
FEATURES	source	Location/Qualifiers										
		1. 811										
		/organism="Ceratopteris richardii"										
		/cultivar="Brogan"										
		/db_xref="taxon:49495"										
		/clone="Cr12_8_L21"										
		/clone_lib="Ceratopteris Spore Library"										
		/tissue_type="Gametophyte"										
		/cell_type="Spore"										
		/dev_stage="20 hours after germination initiation"										
		/note="Vector: pCMVSPORT6; EST sequence from cDNA library."										
		cDNA library constructed from mRNA isolated from C. richardii spores that had developed for 20 hours after their germination had been initiated by white light."										
BASE COUNT	250 a	150 c	201 g	207 t	3 others							

Query Match 26.7%; Score 358.8; DB 10; Length 811;
 Best Local Similarity 65.4%; Pred. No. 4.9e-65;
 Matches 522; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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OY 352 GGAATGAGAGACAGACGCGGAGTTGAGGAAAGGCCAAGGAGATTCCCGACGACTAT 411
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Db 2 GGAATCCCTGAGATGAGTTAAAGAACTGAGACACCGTGGCAGCAATTAACCGATGATAC 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 412 TTTTGTGTTAGTTGAGATGATGATCAAGAAAGACACTTCCACATATATATGCTATG 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 CTGTGCTGCTGCTAGGAGGATATGATTAACGAAAGACCCCTTCGACTTATACAGACCATG 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 472 CTCATAGTGTGTAGTATTAAGATGAGATGAGCGGGCTGAGCCCACTGCTTGGCGAATG 531
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Db 122 CTGAAACACTCTGATGAGATGCTGATGATGATGAGACCAAGCCACATCGTGGCGCAGG 181
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OY 532 TGGACATAGGCGCATGAGCTGCCGAAAGAAATAGACATGTGACCTTCATTAAGTACTCT 591
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Db 182 TGGACTGAGACTTGTGACTGCTGAAGAAATAGACATGTGATCTCTGAACCAATATCTT 241
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OY 592 TATTTGCTGGAAGGCTTGTATGAGAAATTTGAGAGACTATTCATATTCATGCGGC 651
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Db 302 TCTGGAATGGAATCCACAACAGAAATAGCCCTTATTTGGTTTCACTATCTACTCTCTT 361
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OY 712 CAGAAAGAGCAACTTCATATCCCATGCCAACAAGCCAGCTGGCCCAACACTACGGC 771
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Db 362 CAAGAAAGAGCAACTTCTGTTCTCAAGGTAATCTGCCAGGCAAGCAAAAGATTGGT 421
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OY 772 GACAAAGACTCGCTCATCATCTGCGCTCCATGCCCTCCAGCAGAAAGCCACGCGCACA 831
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OY 832 GCTTACACACAGATGCTGGAAGAGCTGCTGAGATGACCCCGACACACAGATTAATTC 891
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Db 482 GCATATACAGAGATGTGGAAGAGCTCTTGAACCTGATTCAGATGACACTATACCTGCT 541
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OY 892 TTTGCAATATGATGCGCAAAAAAATAACATCCAGCGCACTTATGATGACGCGAGT 951
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Db 542 TTAGAGAGATGATGAGAAAGAAATATCCATGCTCCGACACCTGATGATGATGCGCAAT 601
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Db 602 CATAGAGAACTCTTTCACAAATTTCTCTGTGTTGACAAAGGACAGAGAGTACACTGCT 661
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OY 1132 AGCGCAGTGAAGAGAAA 1149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 10
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 LOCUS s13908.y1 Gm-r1030 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-r1030-1336 5' similar to SW:STAD_SOYBN 042807 ACYL-[ACYL-CARRIER
 PROTEIN] DESATURASE PRECURSOR ;, mRNA sequence.
 ACCESSION AWS09087
 VERSION AWS09087.1 GI:7147165
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max

REFERENCE
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuk
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mccann
 R., Waterson,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished (1999)
 JOURNAL Contact: Shoemaker R/Public Soybean EST Project
 COMMENT Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccu@resgen.com
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 Location/Qualifiers
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 /clone="GENOME SYSTEMS CLONE ID: Gm-r1030-1336"
 /clone_1ib="Gm-r1030"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
 cDNA library was constructed from mRNA isolated from
 immature cotyledons of greenhouse grown plants
 (individual seed fresh weight of 100-300mg). The library
 was prepared using the Life Technologies pSuperScript cDNA
 library construction kit. Complementary DNA was
 synthesized from mRNA using a poly(dT) sequence with a
 NotI restriction site. SalI linkers adapters were ligated
 to the blunt-ended cDNA fragments followed by NotI
 digestion. The cDNA fragments were directionally cloned
 into the NotI-SalI restriction site of the pSPORT1
 vector. The ligated cDNA fragments were transformed into
 E. coli Electromax DH10B host cells. This library was
 constructed by Dr. Lila Vodkin and Dr. Ann Khanna. Note
 that Gm-r1030 is a re-track of Gm-cl007."

BASE COUNT 187 a 126 c 163 g 152 t
 ORIGIN

Query Match 26.4%; Score 355; DB 10; Length 628;
 Best Local Similarity 72.9%; Pred. No. 3.1e-64;
 Matches 457; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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OY 321 ACAAGACTACTCCGAGCCGCTGTCAGACGAGATTCGAGAGCAAGTGGGAGTTGAG 380
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Db 1 ACAGAGATTTTACCCGACCCCTCCCTCAGATGATTTGAAGACGAATGAAGAACTGAG 60
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OY 381 GGAAGGCGCCAGAGAGATTCGACGACATATTTTGTGTGTTAGTTGGAGATATGATCAC 440
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Db 61 AGAGAGAGCAAAAGAGATTCAGATGATTTGTTGTGTTCTGTGGAGACATGATGATCAC 120
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OY 441 AGAAGAAAGCACTTCACAAATATATGCTATGCTCAATAGTGTGATGCTTTAAGATGA 500
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Db 121 AGAGGAAGCTCTGCTTACCAACTATGTTAAATATCTTGAATGAGACTTGTGATGTA 180
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OY 501 GACTGGGCGCTGAGCCAGCTGCTGCAAGTGTGAGTGAAGGAGTGCAGCAAGAGAA 560
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Db 181 AACAGGTGCGAGCGCTTACTCTCGGGCAATTTGGACAAGGCGATGACATGCTTAAGAAA 240
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OY 561 TAGACATGTGACCTTCTCAATTAAGTACTTTATTTGTCTGGAAGGTTGATATGAGGAA 620
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Db 241 CAGACACGGTATCTTCTTAACAAATATATCTGTACTGAGTGGAGAGTTCACATGAACA 300
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QY	621	AATGATGAAGACATATTCAATATCTCATGTGGGCTCAGAGATGATATCAAGTCAGAAACAG	680
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QY	681	CCCCCTACCTAGGCTTCATCTACATCTCCCTCCAGAGAGAACCTTCATATTCCTCATGC	740
Db	361	CCCCCTACCTTGGTTTCACTTATTACACTTCTTTCAGAGAGGGCACCCTTCATATTCCTCAGG	420
QY	741	CAACACAGCCCAAGCTGGGCCCAACACTACGCGCGACAAGAACCTCGCTCAACTTCGCGCTC	800
Db	421	AAACACAGCGCAGACCTTGGGAAGAGACATGTGTGCATATAAATTTGGCACAAGATCTCGGCGAT	480
QY	801	CATGCCCTCCAGCAGAGAGCGCCACGCCACAGCCTTACACACAAATGTCTGTGGAAACCTCGC	860
Db	481	GATTTCCTCTAGATGTGGAAGCGCCGACAGACATCTGCATACCAAAAGATGTGGAAACCTGTG	540
QY	861	TGAGATTCACACCCCGCACACACAGTAAATTCCTTTTCAGATATGATGCCCAAAAATATAC	920
Db	541	TGAGGCTGATCTGTATGTGTACAGTTATGTGGCATTTTCCGACATGATGAGAGAGACATTGC	600
QY	921	AATGCCAGCGCAGCTTGTATGTACGACGG	947
Db	601	TATGCCAGCACACCTATGTATGACGG	627
RESULT 11			
LOCUS	B0510820	852 bp	linear EST 22-JUL-2002
DEFINITION	EST618235	Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues	Solanum tuberosum cDNA clone STMN19 5', end, mRNA sequence.
ACCESSION	B0510820		
VERSION	B0510820.2	GI:21926503	
KEYWORDS	EST.		
ORGANISM	Solanum tuberosum		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
SOURCE			
BASE COUNT	236 a	184 c	208 g 224 t
ORIGIN			

Query Match	26.3%	Score 353.4	DB 14	Length 852
Best Local Similarity	73.1%	Pred. No. 6.6e-64		
Matches 467	Conservative 0	Mismatches 171	Indels 1	Gaps 1
Qy	ATCTTCAGTCACACACACATCTATGCGCACCCCAAAACCTGAAATATATCAAGTCCTTGATG	262		
Db		212		
Qy	ATGTTCAAGTACTACTATTCATTCATGCGCGCCAGAGAAACCGTGAATCTTTTATTTCCCTGCATG	271		
Db		263		
Qy	ATTGGCGTAGGAGAACATGTGTGATTTCACCTCAATCTGTGAGAAATCTTGGCAACC	322		
Db		272		
Qy	GTTGGCGTAGAATATATTTTGGTGACACCTAAAGCCGTGAGAAAGTTGGAGCGCCA	331		
Db		323		
Qy	AAGACTACTTGCCTGCGATCCGGTGTACAGCGATTCGAGAGCAAGTGGCGGATTTGAAGG	382		
Db		332		
Qy	GTGACTTTCTTCCTGATCTCCCTGCCCTGAGAGATTTGAAGACCAAGTCAAGAGCTGGCGG	391		
Db		383		
Qy	AAAGGCGCCAGAGATTCCTCCGACCTATTTTGTGGTGTAGTTGGAGATATGATACAG	442		
Db		392		
Qy	AGAGGTGCAAGAGAAATTTCTGTATGACTCTTTGTTGTATTTAGTTGGAGATATGATACAG	451		
Db		443		
Qy	AAGAAGCTTCCCAACATATATGTCTATGCTCAATAGGTGTGATGTTAAGATGAGA	502		
Db		452		
Qy	AGAGAGCTCTTCCAACTATACAGAACAAATGCTTAACACCCTAGATGAGATGCTGATGAA	511		
Db		503		
Qy	CTGGGGCTGAGAGCCACAGTCTTTGGGCAATGTGAGACTAGAGGCAATGACCTCCGAAGAATA	562		
Db		512		
Qy	CTGGGCCACAGGCTAACTCTTTGGGCTATTTTGGACCAAGGATGGCTCTGCTGAGA	570		
Db		563		
Qy	GACATGGTACCTTCTCAATATAGTACCTTTATTTGTCTGGAAGGCTTGATATGAGAGAA	622		
Db		571		
Qy	GGCATGGTGACCTTCTCAACAAATATTTATATCTTTCTGGAAAGATTTATATGAGCGCAA	630		
Db		623		
Qy	TTGAGAGACTATTCATATATCTCATCGGCTCAGAGATGGATATCAAGTACAGAAAACAGCC	682		
Db		631		
Qy	TTGAAACAACTATCAGTACCTCATTTGGTGTGACGAGATGGATCTCCGACGGAAAAACAAC	690		
Db		683		
Qy	CCCTACCTAGGCTCTCATCTACACATCCCTTCCAAAGACAGCAACCTTCATATCCATGGCA	742		
Db		691		
Qy	CGTATCTGGGTTTATTTTACACTTCTCTTCCCAAGAGAGGGCTACCTCTTCTTATGAGAA	750		
Db		743		
Qy	ACACAGCCACACTGGCGCCCAACATCTACGGCGCAGCAAGACCTCGCTACATCTGCGGCTCCA	802		
Db		751		
Qy	ATACAGCTCGCGCATGCTTAAGGAGCATGGGGACATGATAAACTAGCACAGGTATGTGTATAA	810		
Db		803		
Qy	TCGCTCCGAGAGAGAGCGCACGCGCACAGCCTTACACA	841		
Db		811		
Qy	TTGCTGAGATGAGAGCGCCACGAGACCGCGGTATACCA	849		
Db				
RESULT 12				
LOCUS	BC837910	1055 bp	mRNA	linear
DEFINITION	Zm10.10c08_A Zm10_AAFc ECORC Fusarium graminearum_corn_silk zea			EST 25-MAY-2001
ACCESSION	BC837910			
VERSION	BC837910.1			
KEYWORDS	EST.			
SOURCE	zea mays.			
ORGANISM	zea mays.			
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; PACC Clade: Panicoideae; Andropogoneae: Zea.			
AUTHORS	1 (bases 1 to 1055)			
TITLE	Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Couroux,P., De Moors,A., Hattori,J.I., Quillet,T., Robert,L.S., Singh,J.A, Spott ,D. and Tinker,N.A.			
JOURNAL	Expressed Sequence Tags from Maize Silk Six Hours After Silk Channel Inoculation with Fusarium graminearum			

Bl09. 21, Central Experimental Farm, Ottawa, Ontario, KIA 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harristj@em.agr.ca.

FEATURES

source

Location/Qualifiers
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/organism="Zea mays"
/cultivar="CO388"
/db_xref="taxon:4577"
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/tissue_type="Silk"
/dev_stage="4-5 days post-silk emergence"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Field-grown corn was silk channel-inoculated in the morning (-10 am) with 1 ml of a macroconidial suspension (500,000 spores/ml) of Fusarium graminearum and silk channels were collected and immediately frozen in liquid nitrogen 6 hours later. RNA was extracted from silk tissue between 1 cm below and above the inoculation point in the silk channel, RNA from five silk channels was pooled."

BASE COUNT 279 a 231 c 295 g 246 t 4 others
ORIGIN

Query Match 26.1%; Score 351; DB 12; Length 1055;
Best Local Similarity 68.7%; Pred. No. 2.1e-63;

Matches 496; Conservative 3; Mismatches 214; Indels 9; Gaps 1;

532 TGAGTGGGATGAGTACCTCCGAGAGATAGACATGACCTTCTCATATAGTACTT 591

28 TTGACAGAGGCAATRGACACTGAGAGAACAGCATGTGACCTCTTACAGTACATG 87

592 TATTTGCTGAGAGGTTATATGAGAAATTGAGAAAGCTATTCATATCTCATCGC 651

88 TMCCTTACTGAGGCTGTGACATGAAACAATTGAGAACMCATACATATCTGATTGT 147

652 TCAGGATGATATCAAGTCAAGAAACGCCCTTACTAGGCTTCATCTACATCTTC 711

148 TCCGGAATGATCTCGAATGAGAACACCCCTTCTGTTGCTCTACACATCTTTC 207

712 CAAGAGAGCAACCTTCATATCCATGCCACACAGCCAGCCCAACACTACGCG 771

208 CAAGAAAGGCAACATTTGTGCGATGGAATACCTGCAAGCATGCGCAAGGATGCT 267

772 GACAAAGACCTGCTCACAATGCGGCTCCATCGCTCCGACGAGAAGCGCCACG 831

268 GATCTCAACCTGCGCCAGATATGTGGCAGATAGCAGCGATGAGAAGCGCCACG 327

832 GCCTACCAAGATGTGAAAAAGCTGCTGATGATGACCCGACACACAAAGTAATGCT 891

328 GCCTACCAAGATGTGAAAAAGCTGCTGATGATGACCCGACACACAAAGTAATGCT 387

892 TTTGAGATATGATGCGCAAAAAAATTAACATGCGCAGCCACTTGATACGCGAAGT 951

388 TTTGCGATATGATGAGAAAGATCAGATGCCAGCCCATCTATGTAACGAGGTAAG 447

952 GACGAACCTCTTTTAACATTTACAGCGGTTGCTCAGAGAGTGNNGGTTTATTCGCG 1011

448 GACGACAACTGCTGCGACACTTCAGCGGTCGCGCAGAGAGCTGGGCTCTACACGCC 507

1012 TTGGATTATGGGACATCTTAGAGTTTCTGATGATTAATGGAATGGAAGGCTTAGC 1071

508 AAAGACTAGCGCGACATCTCGAGTTCTGTGCCAGAGGGAATGTGGGAGCTTACA 567

1072 GGGCTGTGCGAGGCGGAGAAAGCGAGAAATATGTGTAATTTGGTCCAGATT 1131

568 GGGCTGTGCGAGGCGGAGAAAGCGAGAAATATGTGTAATTTGGTCCAGATT 627

1132 AGCGAGTGGAGAGAAAGTGCAGGGGAGAGAGAGAAAGGCTGAGCACCCTGTT 1191

Db 628 AGCGGCTGATGATGAGCTCAAGCAGGCGGAGCA-----AGCACCGGTTATT 678

QY 1192 TCTTTCAGCTGATTTTCAATCGGAGTGTGAATATGACAGGAGGAGGATGGA 1251

Db 679 CTTTTCAGTGGTTTATGACCGCAGAGCTGAGCTTAAATCAGAACGCTTAGCAATGTG 738

QY 1252 GG 1253

Db 739 GG 740

RESULT 13

AV914373

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 465; Conservative

0; Mismatches 204; Indels

0; Gaps

0;

QY 306

Db 3

QY 366

Db 63

QY 426

Db 123

QY 486

Db 183

QY 546

Db 243

South Memorial Parkway Huntsville, AL 35801 for further information
call: (800)-533-4363 or contact via email: ccu@esgen.com
High quality sequence stop: 417.
Location/Qualifiers

FEATURES
source

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1..606
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl048-1448"
/lssue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site.1: EcoRI; Site.2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 1 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's Laboratory at Northern
Arizona University."
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BASE COUNT 181 a 128 c 143 g 154 t
ORIGIN

Query Match 25.4%; Score 341.6; DB 10; Length 606;
Best Local Similarity 72.8%; Pred. No. 2e-61;
Matches 440; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

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OY 288 TCACCTCAATCTGTCGGAATCTTGGCAACACAGACTACTGCGGATCCGCTGTC 347
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Db 3 TCATCTTAACCTGTGAAATGTGGCAACACAGATTCTTACCGGATCTTCCCTC 62

OY 348 AGACGGATTGAGGCAAGGCGGAGTTGAGGGAAGCGCCAGAGAGATGCCGACGA 407
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Db 63 TGATGGATTGAGAGCAAGTGAAGAGACTGAGAGAGAGGCAAGGACTTCCAGATGA 122

OY 408 CTATTTGTGTTGTTACTTGGAGATATGATCAGAGAGACACTTCCACATATATGTC 467
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 TTACTTTGTTGTTGTCGAGACATGATCAGAGAGAGCCCTGCTACTTACCAATC 182

OY 468 TATGCTCAATAGTGTGATGATTAAGATGAGACTGGGCTGAGCCAGTGTGGGC 527
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OY 528 AATGAGACTAGGCGATGACGCGAGAGACATGATGATGATGATGATGATGATGATG 587
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Db 243 AATTGGACAGGCGATGACGCTGAGAAAGAAACAGACGCTGATCTTACCAATA 302

OY 588 CTTTATTTGCTGGAAGGTTGATATGAGAAATGAGAACTATTCATATCTCAT 647
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Db 303 TCTTACTTGAATGCTGAGTGAATGAACAAATTGAAAGACATTCAGTACTTAT 362

OY 648 CGGCTCAGAGATGATATCAAGTCAAGAAACGCGCTACCTAGGCTCATACACATC 707
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OY 768 CGGCGACAGAACTGCTCATCTGCGGCTTCATGCGCTCCGACGAGAGAGCCAGC 827
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Db 483 CGGCGATATAAAGTTGCGCCAGAGATGCTGATGATTTGCCCTCAGATGAGATAGCCATGA 542

OY 828 CACAGCCATACAGATGATGAGAAAGTGCCTGATGATGAGACCCGACACACAGTAT 887
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Db 543 GACTGCATACAGAGATAGTGAAGAGTACTCGATGTCGATTCGATGATGATGAT 602
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OY 888 TGCT 891
Db 603 GGCT 606

Search completed: December 2, 2002, 00:40:21
Job time : 2417 secs

GenCore version 5.1.3
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OH nucleic - nucleic search, using sw model

Run on: December 1, 2002, 21:12:16 ; Search time 76 Seconds

(without alignments)
5423.336 Million cell updates/sec

Title: US-09-732-597-1

Perfect score: 1344

Sequence: 1 caaccacagaataataaat.....tttgagtttaagtaaaaaa 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents.NA.*
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5: /cgn2_6/ptodata/2/lna/PCRUS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	613.4	45.6	1309	1 US-07-926-788A-1	Sequence 1, Appl
2	572	42.6	1668	4 US-08-471-791-15	Sequence 15, Appl
3	572	42.6	1668	5 US-08-926-522-3	Sequence 3, Appl
4	572	42.6	1668	5 PCT-US91-01746-15	Sequence 15, Appl
5	522	38.8	1533	1 US-07-721-761A-32	Sequence 32, Appl
6	522	38.8	1533	1 US-07-978-687-32	Sequence 32, Appl
7	522	38.8	1533	1 US-08-471-791-12	Sequence 12, Appl
8	522	38.8	1533	4 US-08-926-522-1	Sequence 1, Appl
9	522	38.8	1533	5 PCT-US91-01746-12	Sequence 12, Appl
10	522	38.8	1533	5 PCT-US91-05801-32	Sequence 32, Appl
11	521.2	38.8	2243	1 US-07-995-657-1	Sequence 1, Appl
12	521.2	38.8	2243	1 US-08-474-587-1	Sequence 1, Appl
13	513	38.2	1621	4 US-08-679-645-1	Sequence 1, Appl
14	511.8	38.1	1495	1 US-08-471-791-19	Sequence 19, Appl
15	511.8	38.1	1495	4 US-08-926-522-5	Sequence 5, Appl
16	511.8	38.1	1495	5 PCT-US91-01746-19	Sequence 19, Appl
17	426.4	31.7	1272	2 US-08-869-137-1	Sequence 1, Appl
18	393.8	29.3	1258	1 US-08-539-798-1	Sequence 1, Appl
19	393.8	29.3	1258	1 US-08-329-560-1	Sequence 1, Appl
20	112	8.3	176	1 US-07-721-761A-34	Sequence 34, Appl
21	112	8.3	176	1 US-07-978-687-34	Sequence 34, Appl
22	112	8.3	176	1 US-08-471-791-18	Sequence 18, Appl
23	112	8.3	176	5 PCT-US91-01746-18	Sequence 18, Appl
24	112	8.3	176	5 PCT-US91-05801-34	Sequence 34, Appl
25	64.8	4.8	7218	1 US-08-232-463-14	Sequence 14, Appl
26	57.6	4.3	143	1 US-08-471-791-43	Sequence 43, Appl
27	57.6	4.3	143	4 US-08-926-522-7	Sequence 7, Appl

28	57.6	4.3	143	5 PCT-US91-01746-43	Sequence 43, Appl
29	40.6	3.0	225	1 US-08-471-791-14	Sequence 14, Appl
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37	40.4	3.0	10596	1 US-07-884-811-15	Sequence 15, Appl
38	40.4	3.0	10596	1 US-07-885-971-15	Sequence 15, Appl
39	40.4	3.0	10596	1 US-08-087-783A-15	Sequence 15, Appl
40	40.4	3.0	10596	1 US-08-194-088B-15	Sequence 15, Appl
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42	40.4	3.0	10596	5 PCT-US93-04648-15	Sequence 15, Appl
43	39	2.9	1856	2 US-08-360-606B-29	Sequence 29, Appl
44	38	2.8	289	4 US-09-007-005-17	Sequence 17, Appl
45	38	2.8	289	4 US-09-244-796-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-07-926-788A-1
; Sequence 1, Application US/07926788A
; Patent No. 5430134
; GENERAL INFORMATION:
; APPLICANT: John B. Ohlroge, Edgar B.
; APPLICANT: Cahoon, John Shanklin,
; TITLE OF INVENTION: A Method For
; TITLE OF INVENTION: Production of Petroselinic Acid and 12
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch, 360 kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS (version 3.3)
; SOFTWARE: wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/926,788A
; FILING DATE: 19920807
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; TELEPHONE/DOCKET NUMBER: MSU 4.1-156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1309 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

ORGANISM: Coriandrum sativum
IMMEDIATE SOURCE:
LIBRARY: CDNA
US-07-926-788A-1

Query Match 45.6%; Score 613.4; DB 1; Length 1309;
Best Local Similarity 77.0%; Pred. No. 6.6e-166;
Matches 762; Conservative 0; Mismatches 222; Indels 6; Gaps 1;

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DB 241 GTAGAGAACTCATGSCAGCCGCAACACTATCTGCCGATCCACATCCGATGATTGGA 300
OY 361 GAGCAAGTCCGGAGTTGAGGAAAGGCGCAAGAGATTCGCGACGACTATTTTGTGTG 420
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OY 421 TTAGTTGAGATATATACAGAAAGAGACTTCCAACTATATGTCTATGCTCAATAGG 480
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DB 721 CTAGCTCAAGTGTGGCAACATTTGCTTGTGACGAGAAACGCCATGCCACCGCTACACC 780
OY 841 AAGATCGTGAAGAAAGCTCGCTGAGATCGACCCCGACACACAGATATTTCTTTGCAGAT 900
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DB 781 AAAATCGTGAAGAGCTTCCGAGATGACCCAGACACACAGCTATTTTCATTTCTGAC 840
OY 901 ATGATGCGCAAAAAAATAACATGCCAGCGCACTTGATGATGAGGAGAGTGCAGACT 960
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DB 841 AATGATGAGAAATAATAAATGACAGCTCATGCAATATACCATGCTCCGCAATGATAG 900
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DB 901 CTTTCAAGCACTTCACAGCCGTTGCTCAGCAGATTTGAGATGCTACTCTGATGGATTTAC 960
OY 1021 TGCAGATCTTATGAGTTCGTGATTAATGGAATGTGGAAGGCTTACGGGGCTGTGC 1080
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 961 TGTGACATATATGATTTCTGTGGATTAATGGAACGTTGCGAAGATGACAGGGGCTGTC 1020
OY 1081 GACGAGGGGCGAAAAAGCGAGAAATGTGTGATTTGGGTCGCCAAGATTTAGCCAGT 1140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1021 GGTGAGAGGAGAGAGCTCAAGAAATGTTTGTAGCTTGCGTCTAGATCAGAGAGATT 1080
OY 1141 GAAGAGAAAGTGCAGGAGAGAGAGAGAAAGTGAAGAGTGAAGCCTGTTTTCAGC 1200
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DB 1081 GAGGAGAAAGTTCAAGCAAGC-----AGAGAAAGCTGTGTGCTGTGGCTTTTCAGC 1134
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OY 1201 TGGATTTTCATCGGAGTTGGAATATGA 1230
DB 1135 TGGATTTTCACCGTCAATCATCATATGA 1164

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RESULT 2
US-08-471-791-15
; Sequence 15, Application US/08471791
; Patent No. 5723595
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
; APPLICANT: Knaut, Vic C
; TITLE OF INVENTION: Plant Desaturases-Compositions
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoftword 5.1 (a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,791
; FILING DATE: 6-JUNE-95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01746
; FILING DATE: 14-MAR-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/615,784
; FILING DATE: 14-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/567,373
; FILING DATE: 13-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/494,106
; FILING DATE: 16-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lassen, Elizabeth
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schmedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE 69-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; TELEX: 350370 CGNE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1668 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; US-08-471-791-15
Query Match 42.6%; Score 572; DB 1; Length 1668;
Best Local Similarity 69.1%; Pred. No. 5.4e-154;
Matches 823; Conservative 0; Mismatches 341; Indels 27; Gaps 2;
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Db 89 ACCATGGCCACTACCACTCCCTTAAGTTCTACATGGCTCTACCCCTCAAGCTTGTTG 148
QY 171 CATGGTCTGTATATCTCAAAAGTCC-----GCCAATCTTCAAGT 212
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QY 213 CACTCACTCTATGCCACCCCAAAAGCTAGAAATATTCAAAGTCCCTTGATGTGGGCTAG 272
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QY 453 TCCAAATATATGCTATGCTCAATAGTGTGATGTTAAAGATGAGACTGGGCTGA 512
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Db 449 TCCCACTTATCAAAACAATGCTCAATACCTTGATGATGAGTTCCGGATGAAACAGTCTCAAG 508
QY 513 GCCCAGTGGTGGCAATGGGACTAGGACTGAGTGGCGGAAGAAATAGACATGTTGA 572
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Db 509 TCCCTACTTCTGGCAATTTGACAGAGGCAATGAGTGGGAGAAATAGACATGTTGA 568
QY 573 CCTTCTCAATAGTACCTTTATTTGTCTGCAAGGGTTGATGAGGAAATGAGAAAG 632
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Db 569 CCTCTCAATAGTATCTCTACTCTATCTGAGAGAGTGCATGAGCAATGAGCAATGAGAAAG 628
QY 633 TATTCATATCTCATGCTGCTCAGAAATGATTCAGAGTAGAAACAGCCCTACTAGG 692
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Db 629 AATTCATATTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 688
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QY 753 GCTGGCCCAACTAGAGGCAAGAAACCTGCTCATCTGCGGCTCCATGCCCTCCGA 812
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Db 809 TGAGAAAGCCCATGAGACAGCTACACAAAGATAGTGAAGAAACCTTTGAGATGATCC 868
QY 873 GGACACAAAGTAATTTGCTTTGAGATATGATGCCCAAAAAATTAACATGCCAGCGA 932
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Db 869 TGATGAACTGTTTGGCTTTGCTGTATGATGAGAGAAATTTCTATGCTCTCACA 928
QY 933 CTTCATCTACGAGAGAGTACCACTCTTTTAAACATTTTCACGGGCTTCTGAGAG 992
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Db 929 CTTCATCTACGAGAGAGTACCACTCTTTTAAACATTTTCACGGGCTTCTGAGAG 988
QY 993 ACTGAGGCTTTTCTGCTTGGATTTATGCGACATCTTGAAGTCTTCTGATGAATG 1052
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QY 1053 GAATGGAGAAAGCTTAGAGGGGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1112
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Db 1049 GAGAGTGGATTAACCTAGAGGCTTTCACTGAGGAGCAAAAGGCTGAGAGCTATGTTG 1108
QY 1113 TGAATTTGGTCCCAAGATGAGGAGTGAAGAGAAAGTGCAGGAGGAGGAGGAGGAGGAG 1172
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QY 1173 GAAAGCTGAGCACTGTTTCTTTTCACTGATTTTCAATCGGAGCTGAGATATGAGAC 1232
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Db 1164 -----GAAGCACCCACCATGCTTTTCAGCTGATTTTGCATAGGCAAGTGTAGGT 1219
QY 1233 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1220 GCCTAAAGTCCAGACCAACCAAGATGTTAGTTTCATCTTTTTCATGTC 1270

RESULT 3
US-08-926-522-3
; Sequence 3, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vic C. Knauf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(e)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,522
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/458,173
; FILING DATE: 2-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE DES
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1668 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; US-08-926-522-3

Query Match 42.6%; Score 572; DB 4; Length 1668;
Best Local Similarity 69.1%; Pred. No. 5,4e-154;
Matches 823; Conservative 0; Mismatches 341; Indels 27; Gaps 2;
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Db	269	GGAAACATTTCTGGTTTCATCTGAAAGCCAGTGTGGAAATGTTTGGCAACCCAGATTTT	328
Qy	333	GCCGGATTCGGGTGTCAAGCGAATTCAGAGCAAGTTCGGGAGTTGAGGAAAGGCCAA	392
Db	329	GCCAGATCCCGCCCTCATGATGATTTGTATGAGCAAGTCAAGGAACCTCAGGAGAGCAAA	388
Qy	393	GGAAATTCGCCAGCACTAATTTTGGGTGTAGTTAGATATGATCAGCAAGAACCT	452
Db	389	GGAAATTCCTGATGATATTTTGTGTTTGGTTGGAGACATGATATACGGAAGAACCTT	448
Qy	453	TCCAACTATATGTCTATGCTCAATAGTGTGTATTAAGATGAGACTGGGGCTGA	512
Db	449	TCCCACTTATCAACCATGCTGAATACCTTGATGAGATTGGGATGAAACAGGTGCAAG	508
Qy	513	GCCAGTCTTGGGCATATGAGCATAGGCGATGAGCTGCCGAAAGAAATATGACATGTGA	572
Db	509	TCCACTTCTTGGGCAATTTTGGACAAAGGCGATGAGCTCGGGAAGAAATATGACATGTGA	568
Qy	573	CCTTCTCAATTAAGTACCTTTATTTGTGTGAAAGGTTGTATGATGAGAAATTTGAGAAC	632
Db	569	CCTCTCATATAGTATCTTAACCTATCTGTGACAGAGTGGACATGTGACCAATTTGAGAAC	628
Qy	633	TATTCATATCTCATCGGCTCAGGATGATATCAAGTCAAGAAACAGCCCTACCTAG	692
Db	629	AATTCAAATTTTGGATTGGTTCCAGAAATGATTCACAGCAAGAAACAGTCCATCTTGG	688
Qy	693	CTTCACTACACATCTCTTCCAAAGAGAGAGAACCTTCATATCCCATGCCAACACAGCAA	752
Db	689	GTTCACTATATCAATCATTTCCAGGAAGGCAACCTTCATTTCTCATGGGAACACTGCCG	748
Qy	753	GCTGCCCCAACACTAAGGCGCAAGAAACATCTGCTACATCTGCGCTCCATCGCCTCGA	812
Db	749	ACAACCCAAAGAGATGAGACATTAAGCTTGGCTCAAAATGTGTATCAATGCTGTCAGA	808
Qy	813	CGAAGAGGCCAGCCGACAGGCTTCACCAAGATCTGTGAAAGCAACCTCGTGAATGCAGCC	872
Db	809	TGAGAGGCGCAATGAGAGGCTTACACAAAGATATGTGAAAAACCTCTTTGAGATTGATCC	868
Qy	873	GCACACACACTAATTTGCTTTTGGCATATGATGCGCAAAAAAATAACAATGCCAGCGCA	932
Db	869	TGATGAGACTGTTTGGCTTTTGGCTGATATGATGAGAAAGAAATTTCTATGCTCTACA	928
Qy	933	CTTGATATACAGAGAACTGACAACTCTCTTTTAAACATTTACCGCGGTTGCTCTAGAG	992
Db	929	CTTGATATGATATGAGCCGAGATGATATCTTTTGGACCACTTTTCAAGCTGTGCGAGGG	988
Qy	993	AGTGAAGGTTTATTTCTGCGTTGATATTTTACGACATTTAGAGTTTCTGGTGATAAATG	1052
Db	989	TCTTGAGTCTACACAGAAAGATTTATGCAATATTTGAGATTTCTGGTGGCGAGATG	1044
Qy	1053	GAATGTGAAAGGCTTACGGGGCTGTGAGACGAGGGCGAAAGCCGAGATATGTG	1112
Db	1049	GAGGTGATTAACCTTAACGGGCTTTTACGCTGAGGGCAAAAGGCTCAGGACATTTTGG	1100
Qy	1113	TGAATTTGGTCCCAAGATTTAGGCGAGTGGAGAAAGAAAGTCCAGGGAGAGAGAAAGAA	1172
Db	1109	TGCGTTACCTCCAGATTTAAAGGCTGGAAGAGAGAGCTCAAGGAAGGCAAG-----	1166
Qy	1173	GAAGCTGAGCAACCTGTTTCTTTCAGCTGAGATTTCAATCGGAGTTGAAGATTAAGC	1232
Db	1164	----GAGAGACCACCATGCTCTTTCAGCTGATTTTGCATAGGCAAGTGAAGCTGTAGGT	1212
Qy	1233	AGGAAGGAGGAATGAGAGAGCAAAATGACTGTAGTATGATTTCTATATGC	1283
Db	1220	GCCTAAAGTGCAGAGCAAAACGAAATGGTTAGTTTCACTCTTTTTCATGC	1270

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RESULT 4
PCR-US91-01746-15
; Sequence 15, Application PC/TUS9101746
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
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1      APPLICANT: Knauf, Vic C
2      TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
3      NUMBER OF SEQUENCES: 43
4      CORRESPONDENCE ADDRESS:
5      ADDRESSEE: Calgene, Inc.
6      STREET: 1920 Fifth Street
7      CITY: Davis
8      STATE: California
9      COUNTRY: USA
10     ZIP: 95616
11
12     COMPUTER READABLE FORM:
13     MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
14     COMPUTER: Apple Macintosh
15     OPERATING SYSTEM: Macintosh 6.0.7
16     SOFTWARE: Microsoftword 4.0
17
18     CURRENT APPLICATION DATA:
19     APPLICATION NUMBER: PCT/US91/01746
20     FILING DATE: 19910314
21
22     CLASSIFICATION: 435
23
24     PRIOR APPLICATION DATA:
25     APPLICATION NUMBER: 07/615,784
26     FILING DATE: 14-NOV-1990
27     APPLICATION NUMBER: 07/567,373
28     FILING DATE: 13-AUG-1990
29     APPLICATION NUMBER: 07/494,106
30     FILING DATE: 16-MAR-1990
31
32     ATTORNEY/AGENT INFORMATION:
33     NAME: Lassen, Elizabeth
34     REGISTRATION NUMBER: 31,845
35     NAME: Donna E. Scherer
36     REGISTRATION NUMBER: 34,719
37     REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
38
39     TELECOMMUNICATION INFORMATION:
40     TELEPHONE: (916) 733-6313
41     TELEFAX: (916) 753-1510
42     TELEX: 350370 CGNE
43
44     INFORMATION FOR SEQ ID NO: 15:
45     SEQUENCE CHARACTERISTICS:
46     LENGTH: 1668 base pairs
47     TYPE: NUCLEIC ACID
48     STRANDEDNESS: double
49     TOPOLOGY: linear
50
51     MOLECULE TYPE: cDNA to mRNA
52
53     PCT-US91-01746-15

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Query Match	42.6%	Score 57.2	DB 5	Length 1668
Best Local Similarity	69.1%	Pred. 0.5	4e-154	
Matches	823	Conservative	0	Mismatches 341; Indels 27; Gaps 2
QY	111	ACCACTGACCAAGTAGCTCTCCAAAGGGTTTTCATGGCTTCCACTGTCACTCTAACTC	170	
DB	89	ACCAATGGCGCACTACCAAGATCTCTTAAGTTTCACTATGGCTCTACCCCTCAAGTCGTGTT	148	
QY	171	CATGCTTCTGTAATCTCAAAAGTCC-----GCCAAATCTTCAAGT	212	
DB	149	TAAAGGAAGTTGGAATCTCCAGAAGCCTTTCATGCTCTCCGGAGGTTCATGTTCAAGT	208	
QY	213	CACCTACCTATGCCACCCCAAAAGCTACAATATTCAAGTCCCTGATGTTGGGCTAG	272	
DB	209	TACCAATCTTATGCCACCCCAAAAGTTGAGATCTTTTAATCCCTTAGACAAATTTGGGCTCA	268	
QY	273	GAAACATGTGTTGATTCACCTCAAAATCTGTCGAGAAATTTGGCAACCACAAGACTACTT	332	
DB	269	GGAGAACATCTTGTTGTTCACTCTGACGCCAATTGAGAAATTTGGCAACGCCAGAGATTTTTT	328	
QY	333	GGCGGATCCGGTGTGACAGGATTCGAGGAGCAGAGTCCGGAGTTGAGGAAAAGGCCAA	392	
DB	329	GCCAGATCCCGCTCTGATGAGATTGATGAGCAAGTCAGAGAACCTCAGGAGAGACAA	388	
QY	393	GGAGATCTCCGAGACGACTATTTTGTGTGTTTACTTGGAGATATGATACAGAGAAAGCACT	452	
DB	389	GGAGATCTCTGATGATTAATTTTGTGTTTGGTTGGAGCATGATATACGGAAAGAACCCCT	448	


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1006 TCTCGTGGTATTCGCGCATCTTAAGATTTCTGCTGCGATTAATAATGAAATGTGGAAGG 1065
1081 ACCGCCAAGACHTACGCCCGCATCTGGAATTTCTGCTGCGCGGTGGGAAGTGGCGAT 1140
1066 CTYACGGGGCTGTGCGACGAGGGGCGAAAAAGCGCAGGAATATGTCTGAAATTGGGTCC 1125
1126 AAGTATGGCGAGTGTGGAAGAAAGTTCAGGGGGAAGAGAAACAAAGACAGCTGAGCAC 1185
1201 AGAATCGAAGAGGCTGTGGAGGAGAGAGCTCAAGGGCGAGCAAA- - - - -GAAAGACT 1251
1186 CCGTCTTCTTCTACGCTGATTTTCAATCGGAGGTGAAGATATGAATCAAGAGGAAGG 1244
1252 GTTCTTCATTTCACTGCTGATTTTTCATATAGACAGGTGAAGCTGTGAAGAAAAAAGG 1310

RESULT 7
US-08-471-791-12
Sequence 12, Application US/08471791
Patent No. 5723595
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knaut, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoftword 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,791
FILING DATE: 6-JUNE-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/762,762
FILING DATE: 16-SEPT-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 14-MAR-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 69-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEO ID NO: 12:

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; ORIGINAL SOURCE:
; ORGANISM: Glycine max
; STRAIN: Cultivar Wye
; DEVELOPMENTAL STAGE: Developing seeds
; IMMEDIATE SOURCE:
; LIBRARY: cDNA to mRNA
; CLONE: pDS1
; FEATURE:
; NAME/KEY: 5' non-coding sequence
; LOCATION: 1..69
; OTHER INFORMATION: /note="IDENTIFICATION
; OTHER INFORMATION: METHOD=deduced by proximity to location 70-72"
; FEATURE:
; NAME/KEY: Putative translation initiation codon
; LOCATION: 70..72
; OTHER INFORMATION: /note="IDENTIFICATION
; OTHER INFORMATION: METHOD=Similarity of the context of the
; OTHER INFORMATION: methionine codon in the open reading frame to
; OTHER INFORMATION: translation
; FEATURE:
; NAME/KEY: Putative transit peptide coding sequence
; LOCATION: 70..165
; OTHER INFORMATION: /note="IDENTIFICATION
; OTHER INFORMATION: METHOD=deduced by proximity to location 70-72
; OTHER INFORMATION: and location 166-1242"
; FEATURE:
; NAME/KEY: Mature protein coding sequence
; LOCATION: 166..1242
; OTHER INFORMATION: /note="IDENTIFICATION
; OTHER INFORMATION: METHOD=Experimental determination of N-terminal
; OTHER INFORMATION: amino acid sequence and subunit size of
; OTHER INFORMATION: purified soybean
; FEATURE:
; NAME/KEY: Translation termination codon
; LOCATION: 1243..1245
; OTHER INFORMATION: /note="IDENTIFICATION
; OTHER INFORMATION: METHOD=The translation codon ends the open
; OTHER INFORMATION: reading frame for a protein of the expected
; OTHER INFORMATION: size"
; FEATURE:
; NAME/KEY: 3' non-coding sequence
; LOCATION: 1246..2243
; OTHER INFORMATION: /note="IDENTIFICATION
; OTHER INFORMATION: METHOD=Established by proximity to location
; OTHER INFORMATION: 1243-1245"
; OTHER INFORMATION: 1243-1245"
US-07-995-657-1

Query Match      38.8%; Score 521.2; DB 1; Length 2243;
Best Local Similarity 68.5%; Pred. No. 2.2e-139;
Matches 743; Conservative 0; Mismatches 324; Indels 18; Gaps 1;

OY 112 CCAGTACAGAGATTGCTCCAGAGGTTTTCACCTCCACCTCACTCACTCACTC 171
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 118 CAATGCCAGCTCAGATCTCCCGCTTCGCGATGCGCTCCCGCTCCGCTCC 177

OY 172 ATGCTTTGTATATCTCAAAAGTCGCCAA-----ATCTTCAAGTC 213
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 178 AAAGAGCTGAATAATTAAGAACCATTCACCTCCAGAGAGATGTTTCAAGTA 237

OY 214 ACTCACTATAGCCACCAAAAGCTAGAAATTTCAAGTCCCTTGATTTGGGCTAGG 273
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 238 ACCCACTCTATGCTCCCGAGAGATTGAGATTTCAAATCTTTGAGAGATTGGGCTGAC 297

OY 274 AACCAATGTGTGATTCACCTCAATCTGTCGAGAATCTTGGACACCAAGACTACTTG 333
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 298 CAGAACATCTGTGCTATCTTAACCTGTAGAAAATGTTGGACACACAGATTTTGA 357

OY 334 CCGAGTCGGGTGTGAGAGCGATTGAGAGCAAGTCGCGGAGTTGAGGGAAGGCCCAAG 393
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 358 CCCGACCCCTCCCTCAGATGATTGGAAGCAAGTGAAGACTGAGAGAGAGCAAG 417

OY 394 GAGATTCGCGAGACATATTGTTGGTGTAGTTGAGATATGATCAAGAAAGCACTT 453
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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DB 418 GAGATTCGAGATGATTACTTTGTTGTTCTGTGCGAGACATGATCAAGAGAAAGCTCTG 477
OY 454 CCACATATATGTCATGCTCAATAGGTGTGATGTATTAAGATGAGACTGGGGCTGAG 513
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 478 CTTACTTACCAACTATATGTTAAATACTTGTGATGAGACTGTGATGAACAGCTGCGAGC 537
OY 514 CCGAGTCTTGCGCAANTGTGACTAGGGCATGAGCTCCGCAAGAAATTAACATGTGTGAC 573
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 538 CTTACTTCCGCGGCAATTTTGGACAGAGGCGATGAGCTGTCTAAGAAACACAGCGGTGAT 597
OY 574 CTTCTCAATATAGTACCTTTATTTGTCTGAAAGGTTGATATGAGAAATTTGAAGACT 633
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 598 CTTCTTAACAATATCTGTACTTGTAGTGACAGATTACATGAACAATTTGAGAAAGACA 657
OY 634 ATTCAATATCTCATCGGCTCAGGANTGATATCAAGTCAGAAAAACGCCCTACTAGGC 693
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 658 ATTACAGTACCTTATTTGGGTGTGGATGTGATCTCGACCGAAGAACCCCTACCTTGTGT 717
OY 694 TTGATCTACACATCTTTCCAGAGAGAGCAACCTTCAATTCCTCATGCGCAACAGCCCAAG 753
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 718 TTGATTTACACTTCATTTTCAAGAGAGGCAACCTTCATATCCACAGAAACAGCGCGCAGG 777
OY 754 CTGGCCCAACTAGCGGCGCAAGAACCTGCTCACATCTGCGGCTGCATGCGCTCCGAC 813
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 778 CTTGCGAAGAGCAGTGTGTGACATTAATTTGGCACAGATCTGCGCATGATTTGCTCGAT 837
OY 814 GAGAAAGCGCCAGCGCACAGGCTACACCAGATGCTGGAAGAAAGCTCGCTGAGATGAGCC 873
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 838 GAGAGAGGCGCACGAGACTGCATACACAAGATAGTGAAGAAAGCTTTGAGGTGATGCT 897
OY 874 GACACACAGTAATTTGCTTTGAGATATGATGCGCAAAAAATTAACATGCCAGCCAC 933
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 898 GATGCTACAGTATGAGCTATTTGCCGACATGATGAGAAAGATGCTATGCGCAGCACAC 957
OY 934 TTGATGACGAGGAAAGTGAAGTCTTTTAAACATTTACGCGGTTGCTCAAGAGA 993
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DB 958 CTTATGTATATACGCGCCGCGACGACACCTGTTGATATCTGCTGCGTGCGCACGCGC 1017
OY 994 GTGNGGTTTATTTCTGCTGATTTAGGACATCTTTAGAGTTTCTGTGTGATTAATG 1053
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DB 1018 ATTGGGTTTACACTGCAAGAGACTATGCTGACATCTGCAATTTCTGTGTGGGAGGTGG 1077
OY 1054 AATGTGAAAGGCTTACGGGCTGTGCGACGAGGGGGAAGCGCAGAAATATGTGTGT 1113
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1078 AAGGTGAGCAGCTAACCGGACTTTCAGTGAGGAGAAAGGCTCAGGATACGTTTGT 1137
OY 1114 GAATGGGTCGCCAAGATTAGCGGAGTGAAGAGAAAGTGCAGGGGGAAGGAAGCAAG 1173
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1138 GGGCTGCCACCAAGAAATCAGAAAGGTTGGAGAGAGAGCTCAAGCAAGCAAGCAAGTGC 1197
OY 1174 AAAGC 1178
DB 1198 TCAGC 1202

RESULT 12
US-08-474-587-1
; Sequence 1, Application US/08474587
; Patent No. 5760206
; GENERAL INFORMATION:
; APPLICANT: Hitz, William D.
; APPLICANT: Yaday, Narendra S.
; APPLICANT: Perez-Grau, Luis
; TITLE OF INVENTION: Nucleotide sequence of
; Patent No. 5760206
; TITLE OF INVENTION: Soybean Stearoyl-ACP
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours
; ADDRESSEE: and Company
; STREET: 1007 Market Street
; CITY: Wilmington
```

STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,587
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SIEGEL, BARBARA C.
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB_1022-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2243 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: glycine max
STRAIN: Cultivar Wye
DEVELOPMENTAL STAGE: Developing seeds
IMMEDIATE SOURCE:
LIBRARY: cDNA to mRNA
CLONE: pDS1
FEATURE:
NAME/KEY: 5' non-coding sequence
LOCATION: 1..69
OTHER INFORMATION: /note="IDENTIFICATION
METHOD-deduced by proximity
OTHER INFORMATION: to location 70-72"
FEATURE:
NAME/KEY: Putative translation initiation codon
LOCATION: 70..72
OTHER INFORMATION: /note="IDENTIFICATION
METHOD-similarity of the
OTHER INFORMATION: context of the methionine
OTHER INFORMATION: codon in the open reading frame to translation
FEATURE:
NAME/KEY: Putative transit peptide coding sequence
LOCATION: 166..165
OTHER INFORMATION: /note="IDENTIFICATION
METHOD-deduced by proximity
OTHER INFORMATION: to location 70-72 and
OTHER INFORMATION: location 166-1242"
FEATURE:
NAME/KEY: Mature protein coding sequence
LOCATION: 166..1242
OTHER INFORMATION: /note="IDENTIFICATION
METHOD-experimental
OTHER INFORMATION: determination of N-terminal
OTHER INFORMATION: amino acid sequence and subunit size of purified soybean
FEATURE:
NAME/KEY: Translation termination codon
LOCATION: 1243..1245
OTHER INFORMATION: /note="IDENTIFICATION
METHOD=The translation
OTHER INFORMATION: codon ends the open reading
OTHER INFORMATION: frame for a protein of the expected size"

FEATURE:
NAME/KEY: 3' non-coding sequence
LOCATION: 1246..2243
OTHER INFORMATION: /note="IDENTIFICATION
METHOD=Established by
OTHER INFORMATION: proximity to location
OTHER INFORMATION: 1243-1245"
US-08-474-587-1
Query Match 38.8%; Score 521.2; DB 1; Length 2243;
Best Local Similarity 68.5%; Pred. No. 2,2e-139;
Matches 743; Conservative 0; Mismatches 324; Indels 18; Gaps 1;
QY 112 CCAAGTACCAAGAGTTAGCTCCAGGGTTTCAVGGCTTCACTGCACTAAGTCC 171
DB 118 CAATGCCAGCCCTCAGATCTCCCGCTCCGATGCTCCACCTCCGCTCGGTTCC 177
QY 172 ATGGTTCTATATATCTCAAAAGCCGCCAA-----ATCTCAAGTC 213
DB 178 AAGAGGTTGAAAATVTTAAGAGCCATTCATCTCTCCAGAGAAAGTCAATGTTCAAGTA 237
QY 214 ACTCACTCTATGCGCCACCACCAAAAGCTAGAAATATTCAGTCCCTTGATGTTGGGCTAGG 273
DB 238 ACCGACGCTATGCGCTCCGCCAGAAATGAGATTTTCAATCTTTGGAGAAATGGGCTGAC 297
QY 274 AACATGTGTTGATTCACCTCAAAATCTGCGAATAATCTTGGCAACCAAGACTACTTG 333
DB 298 CAGAACATCTTGACTCATCTTAAACCTGTAGAAAATGTTGGCAACCAAGAGATTTTSTA 357
QY 334 CCGGATCCGGTGTGAGAGGATTCGAGAGCAAGTGGCGGATGAGAGGAAAGGCCCAAG 393
DB 358 CCGGACCCCTCTCAGATGATTTGAAGAGCAAGTGAAGAAATGAAAGAGAGAGCAAG 417
QY 394 GAGATTCCCGCAGCACTATTTTGTGTGTTAGTTGGAGATATGATCAGAGAAGACACTT 453
DB 418 GAGATTCCAGATGATTAATCTTTGTTGTTCTGTGGAGAACATGATCAGAGGAAGACTGTG 477
QY 454 CCAACATATATGCTATGCTCAATAGTGTGATGTTAAGATGAGACTGGGCGCTGAG 513
DB 478 CTTACTTACCAAACTATGTTAAATCTTTGATGAGATTCGTGTGAACAGGCTCCAGC 537
QY 514 CCCAGTCTTGGGCAATAGTGCATGAGGCAATGAGCTCCGGAAGATATAGCATGTGAGC 573
DB 538 CTTACTTCTCGGGCAATTTGACAAGGGCAATGACCTCTTAAGAAACACACACGGTGAT 597
QY 574 CTTCTCAATAGTACCTTTATTTGTCGGAAGGTTGATATGAGAAATTTGAGAACT 633
DB 598 CTTCTTAACAATATGCTGATCTTGAGTGGAGCATGATGACATAACAATTTGAGAAACA 657
QY 634 ATTCAATATGCTATGCGCTCAGGAATGATATCAAGTCACAAAACAGCCCTTACCTAGGC 693
DB 658 ATTCACTACCTTATTTGGTCTGGGATGATCTCGGACCAAGAACACCCCTTACCTGGT 717
QY 694 TTCATCTACACATCTTCCACAGAGAGCAACCTTCATATCCCATGCAACACAGCAAG 753
DB 718 TTATTTTACCTTCATTTTCAAGAGAGGCAACCTTCATATCCACGAAACAGGCCAGG 777
QY 754 CTGGCCCAACACTAGCGCGCAAGAAACCTGCTCAATCTGCGCTCCATCAGCCTCGAC 813
DB 778 CTGGCAAGAGAGCATGTGATTAATAATTTGSCACAGATCTGCGCATGATTTGCTCAGAT 837
QY 814 GAGAAGCGCCAGCCACAGCTTACACCAAGATGTGGAAGAAAGTCCGCTAGATGACACC 873
DB 838 GAGAAGCGCCACAGCACTGATACCAAAATAGTGAAGAAAGCTGTTTGAAGTTGATCTT 897
QY 874 GAGACACAGATATTTGCTTTCAGATATGATGATCGCAAAAATAATCAATGACGAGGCA 933
DB 898 GATGATACAGTATATGCAATTTTCCGACATGATAGAGAAAGATTGCTATGCCAGACAC 957
QY 934 TTGATGTACGACGAGAGTACGAACCTTTTAAACATTTACGGCGGTTGCTCAGAGA 993
DB 958 CTTATGTATAGAGCGCGCGACGACAACTGTTTGAATACACTCTGCGCGGACGAGCGC 1017

Db 1258 CCAGAGCAGAGCCAGAA 1275

RESULT 14
US-08-471-791-19

Sequence 19, Application US/08471791

Patent No. 5723595

GENERAL INFORMATION:

APPLICANT: Thompson, Gregory A

APPLICANT: Knauf, Vic C

TITLE OF INVENTION: Plant Desaturases Compositions

TITLE OF INVENTION: and Uses

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Calgene, Inc.

STREET: 1920 Fifth Street

CITY: Davis

STATE: California

COUNTRY: USA

ZIP: 95616

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.1

SOFTWARE: Microsoft Word 5.1 (a)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,791

FILING DATE: 6-JUNE-95

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/762,762

FILING DATE: 16-SEPT-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/01746

FILING DATE: 14-MAR-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/615,784

FILING DATE: 14-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/567,373

FILING DATE: 13-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/494,106

FILING DATE: 16-MAR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Lassen, Elizabeth

REGISTRATION NUMBER: 31,845

NAME: Donna E. Scherer

REGISTRATION NUMBER: 34,719

NAME: Carl J. Schmedler

REGISTRATION NUMBER: 36,924

REFERENCE/DOCKET NUMBER: CGNE 69-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (916) 753-6313

TELEFAX: (916) 753-1510

TELEX: 350370 CGNE

INFORMATION FOR SEQ. ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 1495 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

US-08-471-791-19

Query Match 38.1%; Score 511.8; DB 1; Length 1495;

Best Local Similarity 69.3%; Pred. No. 8.8e-137;

Matches 715; Conservative 0; Mismatches 308; Indels 9; Gaps 1;

QY 206 TTCAAGTCTACTCTATGCGCCAGCCCAAGCTAGAAATATTCAAGTCCCTGATGATT 265

Db 251 TTCAAGTCTCTCATTCATTCAGCCACCCAGAGATCGAATCTTCAAAATCCATGAGACT 310

QY 266 GGGCTAGAACATGTGTGATTCACCTCAATCTGTGAGAAATCTTGACACCAAG 325

Db 311 GGGCCGAGACAGAACCTTCTAAGCTCAAGAGCTGAGAGAGTCTGGAGCCCAAG 370

QY 326 ACTACTTGCCGATCCGGTGTGACAGAGATTCGAGAGCAAGTCCGGAGTTGAGGAAA 385

Db 371 ACTTCTTAACCGACCTTCATCCGATGGGTTGGAAGATCAGATTAGAGCTAAGAGAGA 430

QY 386 GGGCCAGAGAAATTCGCCAGACATATTGTGGTGTAGTTGAGATATTCACAGAG 445

Db 431 GGGCAAGAGAGCTCCGATGATTAACCTGCTGGTGGTGGAGACATGACAGGAA 490

QY 446 AAGCACTTCCAAATATATGTATGCTAATAGTGTGATGATTAAGATGAGACTG 505

Db 491 AGGCGTTCCGACCTATCAATCAACCATGTTGAACACTTTGGATGAGATGAGATGAACTG 550

QY 506 GGGCTGAGCCCAAGTGGTGGCAATGTGACTAGGGCATGGACTGCCAGAGATAAGAC 565

Db 551 GGGCTAGCCCAAGTGGTGGCAATGTGACTAGGGCATGGACTGCCAGAGATAAGAC 610

QY 566 ATGCTGACCTTCTCAATTAAGTACCTTTATTTGTGGAAGGTTGATATGAGAAATG 625

Db 611 ACGGTGATCTTCTCAATTAAGTATCTTACTGTGTGACGTTGACATGAGGAGATG 670

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Db 671 AAGAGACATTCATTAATCTGCGCTGAGATGATGATTAAGTCAAGCAAGACCCCT 730

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Db 731 ACCTAGGCTTCATTAATCTGCGCTGAGATGATGATTAAGTCAAGCAAGACCCCT 790

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Db 791 CAGCTCGCAAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 850

QY 806 CCTCGAG 865

Db 851 CTGACAG 910

QY 866 TCGAAG 925

Db 911 TTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 970

QY 926 CAGCGCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 985

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Db 1091 GGAGGTGAAGATTTGAGAGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1150

QY 1106 ATGTGTGGAATTTGAT 1165

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QY 1166 AGAAGAT 1225

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QY 1226 TATGACAGGAA 1237

Db 1262 TCTAAAGAGAA 1273

RESULT 15


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US-08-926-522-5
; Sequence 5, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
; APPLICANT: Vic C. Knaf
; APPLICANT: Gregory A. Thompson
; TITLE OF INVENTION: PLANT SEED OILS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: CA
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1(a)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,522
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/458,173
; FILING DATE: 2-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; NAME: Carl J. Schwedler
; REGISTRATION NUMBER: 36,924
; REFERENCE/DOCKET NUMBER: CGNE DES
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (916) 753-6313
; TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1495 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-926-522-5

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Query Match      38.1%; Score 511.8; DB 4; Length 1495;
Best Local Similarity 69.3%; Pred. No. 8.8e-137;
Matches 715; Conservative 0; Mismatches 308; Indels 9; Gaps 1;
QY 206 TTCAGTCTACTCTACTATGCTCCACCCCAAAAGCTAGCAATATTCAGTCCCTTGATGATT 265
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QY 326 ACTACTTGGCGGATCCGGTGTCTGAGCGATTCAGAGCAAGTGGGAGATTGAGGAAA 385
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DB 371 ACTTCTTACCCGCTGATCGATGGGTTCGAAAGATCAGGTTAGAGCTTAAGAGAGA 430
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QY 506 GGGCTAAGCCCAATGCTTGGGCAATGTGAGCTAGGAGTGGAGTCCCGAAGAGATAGAC 565
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DB 551 GCGCTAGCCCCACTTCAATGGGCTATTTGGACAGAGACTTGGACTGCGAAGACACCGAC 610
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DB 611 ACGGTGATCTTCTCAATATAGATCTTACTTGTTCTGTGACGCTGATGATGAGAGATTTG 670
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DB 671 AAAAGACCATTCAGTACTTATTTGTTCTGAAATGATCCTAGAACAGAACATCTT 730
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DB 731 ACTCGGCTTCACTTACATCTTCCAGAAAGAGCCCTTATCTCTCAGGAAACA 790
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DB 911 TTGATCTGATGTTAGTGTGATGGGCTTTCAGACATGATGAGAGAGAAATCTCGATTC 970
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DB 971 CTGCTCACTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1030
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QY 1226 TATGACAGGAA 1237
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Search completed: December 2, 2002, 00:41:48
Job time : 84 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 21:12:16 ; Search time 304 Seconds

(without alignments)
9956.203 Million cell updates/sec

Title: US-09-732-597-1

Perfect score: 1344

Sequence: 1 caaccgccagaaataaataat.....ttgagtttaagtaaaaaa 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2165239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002:*

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- 24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	613.4	45.6	1309	AA092889	Coriander omega-12
2	573.8	42.7	1643	AA035667	DNA encoding a ste
3	572	42.6	1668	AA015252	Ricinus communis d
4	568.8	42.3	1668	AA013964	R. communis delta9
5	555.8	41.4	1092	AA084531	Mature castor enzy
6	522	38.8	1533	AA013963	C. tinctorius delt
7	522	38.8	1533	AA022616	Carthamus tinctori
8	522	38.8	1533	AA064003	Sequence encoding
9	522	38.8	1533	AA015250	Carthamus tinctori

10	522	38.8	1533	20	AA035666	DNA encoding a ste
11	521.6	38.8	1524	15	AA055760	Delta-9-desaturase
12	521.4	38.8	1529	18	AA063437	Rapeseed stearyl-
13	521.2	38.8	2243	13	AA020187	Soybean seed stea
14	521.2	38.8	2243	19	AA029236	Nucleotide sequenc
15	516.4	38.4	1553	22	AA022378	Cotton stearyl-AC
16	514.6	38.3	1683	18	AA063438	Rapeseed stearyl-
17	513.6	38.2	1714	21	AA035179	Corn delta-9 stea
18	513.2	38.2	1176	16	AA000397	Stearyl-ACP-desat
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20	513.2	38.2	1342	21	AA042392	Arabidopsis thalia
21	513.2	38.2	1552	16	AA000396	Stearyl-ACP-desat
22	513.2	38.2	1687	21	AA048442	Arabidopsis thalia
23	513.2	38.2	1689	21	AA039517	Arabidopsis thalia
24	513.2	38.2	2243	16	AA000395	Stearyl-ACP-desat
25	513	38.2	1107	21	AA061031	Nucleotide sequenc
26	513	38.2	1621	18	AA062127	Zea mays delta-9 d
27	513	38.2	1621	21	AA061026	Nucleotide sequenc
28	511.8	38.1	1495	12	AA013965	B. campestris delt
29	511.8	38.1	1495	19	AA015253	Brassica campestr
30	509.4	37.9	1080	16	AA000398	Mature stearyl-AC
31	498.8	37.1	1567	21	AA037983	Arabidopsis thalia
32	495.8	36.9	1651	21	AA037494	Arabidopsis thalia
33	489.6	36.4	1709	21	AA035180	Corn delta-9 stea
34	483.4	36.0	1657	17	AA027645	Delta-9-fatty acid
35	428.8	31.9	2751	22	ABA94565	A. thaliana fatty
36	426.6	31.7	1466	22	AA050960	Plastidial delta 9
37	426.4	31.7	1272	20	AA081284	DNA encoding delta
38	415	30.9	1395	21	AA035393	Arabidopsis thalia
39	393.8	29.3	1258	17	AA018906	Delta-6-palmitoyl
40	392.4	29.2	1560	24	AA032889	Soybean diverged d
41	367.6	27.4	1318	24	AA032906	Rice diverged delt
42	362.6	27.0	1415	24	AA032904	Corn diverged delt
43	334.6	24.9	1717	24	AA029242	Plasmaid pB68 2x E
44	303	22.5	1234	21	AA053615	Arabidopsis thalia
45	284.6	21.2	2705	19	AA031999	Flax SMD2 gene. L

ALIGNMENTS

RESULT 1	AA092889	standard; cDNA: 1309 BP.
ID	AA092889	
XX	AC	AA092889;
XX	XX	
DF	05-DEC-1995	(first entry)
XX	XX	
DE	Coriander omega-12 desaturase cDNA.	
XX	XX	
KM	Coriander; omega-12 desaturase; petroselinic acid;	
KW	transgenic plant; crop improvement; tobaccos; ss.	
XX	XX	
OS	Coriandrum sativum.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	7..1164
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PN	US5430134-A.	
XX	PN	
XX	04-JUL-1995.	
PD	PD	
XX	XX	
PF	07-AUG-1992;	92US-0926788.
XX	XX	
PR	07-AUG-1992;	92US-0926788.

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XX (UMNS ) UNIV MICHIGAN STATE.
PA
XX
XX Cahoon EB, Ohlrogge JB, Shanklin J, Somerville CR;
XX
XX WPI; 1995-253884/33.
DR
XX P-PSDB; AAR76578.
XX
XX New omega-12 desaturase from coriander - and DNA encoding it, useful
XX for making transgenic plants able to synthesise petroselinic acid.
XX
XX Disclosure; Columns 17-18; 25pp; English.
XX
XX A cDNA library prep'd. from developing seeds of coriander was
XX screened with a probe based on a partial cDNA clone (AAQ92888) of
XX omega-12 desaturase to isolate full-length clone EC201 (AAQ92889).
XX Expression of this cDNA in transgenic tobacco callus resulted in
XX prodn. of petroselinic acid (18:1 omega 12) and omega-12
XX hexadecenoic acid.
XX
XX
SQ Sequence 1309 BP; 360 A; 280 C; 319 G; 350 T; 0 other;

Query Match 45.6%; Score 613.4; DB 16; Length 1309;
Best Local Similarity 77.0%; Pred. No. 2e-162;
Matches 762; Conservative 0; Mismatches 222; Indels 6; Gaps 1;

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DB 361 CTTGTTGAGACATGATGATCAGTGAAGAGGACATCCCAACTACATGCTATGCTTAA 420
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OY 841 AAGATGTGGAAGAGCTGCGTGATGACCGCGACACACAGAAATTTGTTTGCAGAT 900
DB 781 AAAATGCTGAGAGCTTGGGAGATTGACCCAGACACCCTGTTATCGGATTTTTCGAC 840
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DB 841 ATGATGAGGAAGAAATTAACAAATGCCAGCTCATGCAATGTACGATGGCTCGATGATATG 900
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OY 1081 GAGCAGGCGGGAAGCGGCAAGATATGTTGTAATTTGGGCTCCCAAGATTAGCGAGTG 1140
DB 1021 GGTGAAGGGAAGAGCTCAGATATATGTTGATGCTTGGCTCTAAGATCAGAGAGTT 1080
OY 1141 GAAGAGAAAGTGCAGGGAAGAGAGAAAGAAAGCTGAGCACCCTGTTCTTTCAGC 1200
DB 1081 GAGCAGAGAGTTCAAGGCAAG-----ACAAGAAAGCTGTGTGCTGTGCTTTCAGC 1134
OY 1201 TGGATTTTCAATGGGAGTTGAAGATATGA 1230
DB 1135 TGGATTTTCAACCGTCAGATCATATATGA 1164
```

```
RESULT 2
AAK35667
ID AAK35667 standard; DNA; 1643 BP.
XX
XX AAK35667;
XX
XX 16-JUL-1999 (first entry)
XX
XX DNA encoding a stearyl-acyl carrier protein desaturase.
XX
XX Localised mutation; target gene; plant cell;
XX recombinogenic oligonucleobase; selective growth advantage;
XX herbicide resistance; preservation; fruit; flower; ss.
XX
XX Ricinus communis.
XX
XX WO9907865-A1.
XX
XX 18-FEB-1999.
XX
XX 05-AUG-1998; 98WO-US16267.
XX
XX 05-AUG-1997; 97US-0054836.
XX
XX (KIME-) KIMERAGEN INC.
XX
XX Antzen CJ, Kipp PB, Kumar R, May GD;
XX
XX WPI; 1999-302251/25.
XX
XX Introducing mutations into target genes in plant cells - using a
XX recombinogenic oligonucleobase comprising 2 regions homologous to a
XX target gene and an intervening mutant region
XX
XX Example 5; Page 41; 53pp; English.
XX
XX The specification describes methods for introducing localized mutations
XX into target genes in plant cells. The methods comprise using a
XX recombinogenic oligonucleobase comprising 2 regions homologous to a
XX target gene and an intervening mutant region. The methods can be used
XX to introduce localized mutations into target genes to introduce desirable
XX traits, e.g. selective growth advantage under appropriate selective
XX conditions, change in colour of plant cells growing in a callus,
XX herbicide resistance, or improved preservation of fruit or flowers.
XX They can be used in plants such as maize, wheat, rice, lettuce, potato,
XX tomato, canola, soybean or cotton cell. The present sequence represents
XX a target for the methods of the invention.
XX
XX Sequence 1643 BP; 462 A; 321 C; 383 G; 477 T; 0 other;
XX
XX Query Match 42.7%; Score 573.8; DB 20; Length 1643;
```



```
QY 111 ACCAGTACCAGAGTTAGCTTCCAAAGGGTTTCATGGCTCCAGTCTCACTCACTACTC 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 89 ACCAATGGCCAGACAGATCTCTAAGTTCTACATGGCCCTCTACCTCAAGTCTGGTTTC 148
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 171 CATGTTCTGATTAATCTCAAAAGTCC-----GCCAATCTTTCAGT 212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 149 TAGAGAAAGTTGAATGTCAAGAAAGCTTTTCATGCTCCCTGGGAGGTACATGTTCAAGT 208
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 213 CACTCATCTATGCCACCCCAAAAGCTAGAAATATTCAGTCCCTTGATGATTTGGCTAG 272
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 209 TACCCATCTATGCCACCCCAAAAGATGAGATCTTTAAATCCCTAGACAAATTTGGCTGA 268
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 273 GAACATGTGTTGATTCACCTCAATCTGCGGAAATCTTGGCAACCCACAACACTACTT 332
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 269 GGAGAACATCTGGTTCACTGTGAAGCCAGTTGGAATGTTGGCAACCCGAGATTTTTTT 328
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 333 GCCGATCCGCGTGTACAGAGGATTCGAGAGCAAGTCGGGAGTTGAGGAAAGGCCAA 392
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 329 GCCAGATCCCGCTCTGATGATTTGATGAGCAAGTCAGGAACTCAGGAGAGAGCAAA 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 393 GGAGATTCGCGAGCACTATTTTGTGTAGTTGAGATATGATCAGAGAAAGCACT 452
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 389 GGAGATTCGATGATTAATTTGTTGTTGTTGTTGAGAGACATGATAAGGAAAGCCCT 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 453 TCCACATATATGCTATGCTCAATAGTGTATGTTATTAAGATGAGACTGGGCTGA 512
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 449 TCCCACTTATCAAAACAATCTGTAATCTTGATGAGTTGGGATGCAACAGTCGCAAG 508
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 513 GCCCAGTGTGGGCAATGTGACATGAGGCACTGAGGATGCCGAGAGAAATAGACATGTTGA 572
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 509 TCCCTACTTCTTGGGCAATTTGGACAAGGCGATGACTGCGGAAAGANATGACATGTTGA 568
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 573 CCTTCTCAATTAAGTACTTATTTTGTGTGAGAGGTTGATATGAGAAATTTGAGAGAC 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 569 CCGCTCAATTAAGTACTTCTACTATCTGAGACGATGAGACATGAGCAAAATTTGAGAGAC 528
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 633 TATTCATATCTCATGGGCTCAGAGATGATATCAAGTCAAGAAACAGCCCTACCTAGG 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 629 AATTCATATTTGATGTTGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 588
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 693 CTTCATCTACATCTCTCTCCACAGAGAGACACCTTCATATCCATGCCAACAGCCAA 752
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 689 GTTCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 748
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 753 GCTGGCCCAACACTACGCGCAGCAAGAACTCGCTACATCTGCGGCTCATCGCTCCGA 312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 749 ACAAGCCAAAGACATGAGACATAAAGTTGGCTCAAAATGTGTCATATGCTGCTGAGA 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 813 CGAAGAGCCCGCACGCGCACAGCTACACCAAGATCGTGGAAAAGCTGCTGAGATCCAGCC 372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 809 TGAGAAAGCCGATGAGACAGCCCTACACAAAGATAGTGGAAAACTTTTGAATTTGATCC 368
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 873 CGACACAGAGTAAATGCTTTTTCAGATATGATGCGCAAAAAAATAACATATGCGAGCA 932
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 869 TGATGAACTGTTTGGCTTTTTCATATGATGAGAAAAAATAATTTCTATGCTGACACA 928
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 933 CTTCATGTAAGCAGAGAGTGAAGTCTTTTAAACATTTTCAACGCGGCTGCTCAGAG 992
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 929 CTTCATGTAAGTGAAGGCGGAGATGATATCTTTTGACCACTTTTTCAGCTGTTGGCAGCG 988
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 993 AGTGGGGTTTATTCGCGTGTGATATTCGACATCTTGAAGTCTTGTGATTAATG 1052
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 989 TCTTGAAGTCTACACAGCAAAAGGATATGATATATTTGAGATCTTCTTGTGGCAAGT 1048
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1053 GAATGTGAAGAGCTTACGCGGCTGTGCGAGAGGCGGCAAAAGCCGAGAAATATGTGTG 1112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1049 GAAGTGTGAATTAACAAAGGCGCTTTCAGCTGAGGAGCAAAAGGCTCAGATATGTTTG 1108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1113 TGAATTTGGTCCCAAGATTTAGCGAGTGAAGAGAAAGTCCAGGAGGAGAGAGAAAGAA 1172
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1109 TCGGTTTACGTCCAAAGATTTAGAGGCTGCAAGAGAGAGCTCAAGAGAGGCAAG----- 1163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1173 GAAAGTGAAGCACCTGTTTCTTTCAGCTGATTTTCAATCCGGAGTTGAAGATATGAC 1232
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DB 1164 -----GAAGCACCCACCATGCTTTCACCTGGATTTTGGATAGGCAAGTGAAGTGTAGT 1219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1233 AGGAAGGGAAGGAATGAGAGAGCAATGAGTGTAGTATGATTTCTATATTC 1283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1220 GGCTAAAGTGAAGAGCAAAAGCAAAATGTTAGTTTCACTCTTTTCATGCG 1270
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
AAC84531
ID AAC84531 standard; DNA: 1092 BP.
XX
XX AAC84531;
AC
XX 02-APR-2001 (first entry)
DT
XX
DE Mature castor enzyme encoding DNA.
XX
KW Castor; delta9-18:0-acyl carrier protein desaturase; ACP; enzyme;
KW vegetable oil; fatty acid; nutrition; plant oil; mutant; ds.
XX
OS Ricinus communis.
XX
FH Key Location/Qualifiers
FT CDS 1..1092
FT /tag= a
FT /product= "mature castor enzyme"
XX
PN WC200075170-A1.
XX
PD 14-DEC-2000.
XX
PE 08-JUN-2000; 2000MO-US15741.
XX
PR 09-JUN-1999; 99US-0328550.
XX
PA (BROO-) BROOKHAVEN SCI ASSOC LLC.
XX
PI Shanklin J;
XX
DR WPI: 2001-091202/10.
XX
DR P-PSDB: AABA8199.
XX
PT New mutant castor Delta9-18:0-Acy1 Carrier Protein desaturase, useful
PT in producing commercially valuable products, e.g. vegetable oils useful
PT in human nutrition or as industrial chemicals
XX
PS Example; Fig 1; 53pp; English.
XX
XX The invention relates to a new mutant castor Delta9-18:0-acyl carrier
XX protein (ACP) desaturase that has one or more amino acid substitutions
XX selected from: (a) Ala for Met at residue 114; (b) Arg for Thr at residue
XX 117; (c) Gly for Leu at residue 118; (d) Val for Pro at residue 179; (e)
XX Val for Thr at residue 181; (f) Leu for Gly at residue 188; and (g) Phe
XX for Thr at residue 181. The mutant castor Delta9-18:0-ACP desaturase is
XX useful in producing commercially useful products, such as Vegetable oils
XX rich in monounsaturated fatty acids. Such vegetable oils are important in
XX human nutrition and can be used as renewable sources of industrial
XX chemicals. A method for specifically altering a function of a protein
XX through directed mutagenesis is also provided. The method can be used
XX altering enzymatic functions, binding functions or structural functions
XX of the castor desaturase enzyme. The method is also useful for
XX manipulating the physical properties and commercial uses of conventional
XX plant oils. The present sequence represents the DNA encoding a mature
XX castor enzyme.
XX
SQ Sequence 1092 BP; 318 A; 214 C; 282 G; 278 T; 0 other;
    Query Match 41.4%; Score 555.8; DB 22; Length 1092;
    Best Local Similarity 72.1%; Pred. No. 3.1e-146;
    Matches 741; Conservative 0; Mismatches 278; Indels 9; Gaps 1;
QY 201 AAATCTCAAGTCACTCACTATATGCAACCCCAAAAGCTAGAAATATTTCAAGTCCCTTGA 260
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Db 72 ACATGTTACAGTTACCATTCATGACCCCAAAAGATTAGATCTTTAAATCCCTAGA 131
QY 261 TGTATGGGCTAGAGAACATGTGTGATTCACCTCAATCTGTGAGAAATCTTGGCAACC 320
Db 132 CAATTTGGGCTGAGAGAGAACTGTCTGTCATCTGAAAGCCAGTTGAAATGTGGCAACC 191
QY 321 ACAAGACTACTTCCCGATCCGGTGTACAGAGATTGAGAGCAAACTGCGGAGTTGAG 380
Db 192 GCGAGATTTTTTCCAGATCCCGCTCTGTATGGATTGATGAGACAACTCAGGCACTCAG 251
QY 381 GGAAGGCGCCAGAGATTCCGACGACTATTTTGTGTTAGTTGAGATATGATCAC 440
Db 252 GGAGAGAGCAAAAGAGATTCTGATGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 311
QY 441 AGAAGAGACCTTCCAACTATATGCTATGCTCAATAGTGTGATTTAAGATGA 500
Db 312 GGAAGAGAGCCCTTCCCACTTAAACAAATGCTGAATACCTTGGATGGAGTTGCGGATGA 371
QY 501 GACTGGGGCTGAGCCAGTGTCTGGGCAATGTGAGTACGAGTACGCTGCGGAAGAA 560
Db 372 AACAGGTGCAAGTCCGACGCTTGGGCAATTTGGACAAAGGCACTGCGGAGAGAA 431
QY 561 TAGACATGTGTACCTTCTCAATAAGTACCTTATTTGTCTGGAAGGGTTGATATGAGAA 620
Db 432 TAGACATGTGTACCTTCTCAATAAGTACCTTATTTGTCTGGAAGGGTTGATATGAGAA 491
QY 621 AATTGGAAGACATTTCAATATCTCAATCGGCTGAGAAATGGATATCAAGTCAGAAACAG 680
Db 492 AATTGGAAGACATTTCAATATTTGATGTTGATGAGAAATGGATCCGCGGAGAAACAG 551
QY 681 CCCCTACCTAGGCTTCACTACACATCCCTCAAGAGAGAGCAACCTTCATATCCCATGC 740
Db 552 TCCATACCTTGGGTTGATCATATCATCATTTCCAGAAAGGCAACCTTCATTTCTCATGG 611
QY 741 CAACACAGCCAGCTGCGCCCAACACTAGCGGACAGAAACCTGCTGCATCTCGCGCTC 800
Db 612 GAACACTGCGCCGACAAAGCCAAAGAGCATGAGACATTAAGTGGCTCAAAATATGTGTAC 671
QY 801 CATCGCTCCGAGAGAGAGGCGCACGACGCTACACCAAGATCTGTGAAAAGCTCGC 860
Db 672 AATTGCTGAGATGAGAGAGCGCATGAGACGCTTACACAAAGATTAAGTAAAAAATCTT 731
QY 861 TGAATGACGCCCGACACACAGTAATTTGCTTTCAGATGATGATGGCAAAAAAATTAAC 920
Db 732 TGAATGATGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 791
QY 921 AATGCAAGCGCACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 980
Db 792 TATGCTGACACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 851
QY 981 GGTGCTCAGAGAGTNGGGTTATTTCTGCTTGTGATTTATGCGACTTCTAGAGTTCT 1040
Db 852 TGTGGCGACGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 911
QY 1041 GGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1100
Db 912 GGTGGGAGAGTGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 971
QY 1101 GGAATATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1160
Db 972 GGAATATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1031
QY 1161 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1220
Db 1032 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1082
QY 1221 GAAGATAT 1228
Db 1083 GAAGCTGT 1090

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RESULT 6

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AA013963
ID AA013963 standard; DNA; 1533 BP.
XX
AC AA013963;
XX
DT 11-DEC-1991 (first entry)
XX
DE C. tinctorius delta9 desaturase from pCGN274.
XX
KW Desaturase; probe; ss.
XX
OS Carthamus tinctorius.
XX
FH Key location/Qualifiers
FT CDS 106..1294
FT mat_peptide 106..204
FT mat_peptide 205..1294.
FT mat_peptide /*tag= c
PE 14-MAR-1991; 91MO-U001746.
XX
PD 19-SEP-1991.
XX
PR 14-NOV-1990; 90US-0615784.
PR 16-MAR-1990; 90US-0494106.
PR 13-AUG-1990; 90US-0567373.
XX
PA (CALG-) CALGENE INC.
XX
PI Thompson G, Knauf V;
XX
WP1: 1991-295627/40.
DR P-PDB; AAR14188.
XX
PT DNA encoding a plant desaturase - used for modifying the satd.
PT fatty acid compsn. of plant cells and plant seeds
XX
PS Disclosure; Fig 2; 128bp; English.
XX
CC The cDNA comprises a poly(A) track at the 3' end of 100-200 bases.
CC A desaturase was purified from C. tinctorius and sequenced. Based
CC on this sequence, oligonucleotide probes were synthesised and used to
CC screen a C. tinctorius embryo cDNA library to obtain DNA encoding the
CC desaturase. The DNA for the C. tinctorius desaturase was also used as
CC a probe to isolate DNA encoding desaturase from Ricinus communis
CC (AA013964), Brassica campestris (AA013965) and Simmondsia chinensis
CC (AA013966).
CC See also AA013963-69.
XX
SQ Sequence 1533 BP; 420 A; 327 C; 392 G; 394 T; 0 other;
Query Match 38.8%; Score 522; DB 12; Length 1533;
Best Local Similarity 68.5%; Pred. No. 1.3e-136;
Matches 739; Conservative 0; Mismatches 331; Indels 9; Gaps 1;
QY 166 AACTCAGAGTGTCTGTAATCTCAAAAGTCCGCCAATCTTCAAGTCACTCACTATG 225
Db 241 AATGCCAAGAAAGCTTTTCAACCTCCAGAGAGTTCATGTCAGTGAAGCACTCATG 300
QY 226 CCACCCCAAAAGCTAGAAATATTCAGTCCCTGATGATTTGGCTAGGAACATGTGTTG 285
Db 301 CCACCAAGAAAGATGAGATTTTCAAAATCCATCAGAGGTTGGGCTGAGACATATTTG 360
QY 286 ATTCACTCAAACTGTGCGAAATCTTGGCAACCAACAGACTCTTGGCGGATCGGCTG 345
Db 361 GTTCACCTAAAGCCAGTGTGAGAAATTTTGGCAAGCAGAGATTTTGGCGGACCTGCA 420
QY 346 TCAGACGATTCGAGAGAGAGTGTGAGGAGAAAGGCGCAAGAGAGATTTCCGAC 405

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Db 421 TCTGAAGATTGATGATACAGTCAAGAACTAAGGCAAGACAAAGGATTCCTGAT 480
QY 406 GACTATTTTGTGGTGTAGTGGAGATATGATCCAGAAAGACACTTCCACATATATG 465
Db 481 GATTACTTTGTGTTGTGGATATGATATACAGAGAACCCCTACTACTTACCAA 540
QY 466 TCTATGCTCAATAGTGTATGATATTAAGAGATGAGACTGGGGCTGAGCCACTGCTTG 525
Db 541 ACAATGCTTAATACCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 500
QY 526 GCAATGTGACTAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 585
Db 601 GCTGTGTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 660
QY 586 TACCTTATTTGTGTGAGAGTGGTGTGATATGAGAAATTTGAGAAAGATTTCAATATCT 645
Db 661 TATCTACTCTTCTGGGGGGGTAGACATGAGACATACAGAAAGCAATTCAGTATCTC 720
QY 646 ATCGGCTCAGAAATGATATCAAGTCAAGAAACAGCCCTTACCTAGGCTTCATCTACACA 705
Db 721 ATTTGGTCTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 706 TCCCTTCAGAGAGAGCACTTCATATCCATGCGCAACAGACACCCAGCTGGCCCAAC 765
Db 781 TCGTTTCAAGAGCTGCCACATTTGTTTCTCAGGAAACACCGCCAGGCTGCAAGAGAT 840
QY 766 TACGGGACAGAACTCCGCTCAGATCTCGGCTCCATCGCTCCAGAGAGAGAGAGAT 825
Db 841 CATGGGAGAGTGAATGCGCGCAATTTGTGTATCATGCGCTGACGAAAGCGCTCAC 900
QY 826 GCCACAGCCTTACACCAAGATCTGTGAAAGAGCTGCTGAGATGCAACCCGACACAGTA 885
Db 901 GAGACCGCTTATACCAAGATAGTCAAGAAAGCTATGAGATGATGATGATGATGATGAT 960
QY 886 ATTTGCTTTCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 945
Db 961 CTTCGTTTTCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 946 GGAAGTGAAGAACTTTTAAACATTTTCAAGGCGTTCAGAGAGTGGAGTGTAT 1005
Db 1021 GGGCGGTGATGACAACTCTTTCGAACATTTCTGCGGTTGCCAAAGAGCTGGCGTCTAC 1080
QY 1006 TCTGCGTGTGATATTCGACATCTTAAAGATTTCTGCTGATTAATGAAATGTGAAAG 1065
Db 1081 ACCGCGCAAGAGTACGCGACATCTGGAATTTCTGCTGCGGCGGTGAAAGTGGCGAT 1140
QY 1066 CTTCAGGCGCTGTCGAGAGAGAGGCGGAAAGCGCAGAAATATGATGATGATGATGAT 1125
Db 1141 TTGACCGGCTATCTGTGAAGGCGTAAAGCGCAAGATTATGTTGCGGTTGCCACCA 1200
QY 1126 AAGATTAGCGAGTGAAGAGAAAGTGCAGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1185
Db 1201 AGAATCAGAAAGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1251
QY 1186 CCTGTTTCTTCACTGATTTTCAATCGGAGTGAAGATTAAGATGAGAGAGAGAGAG 1244
Db 1252 GTTGTTCATCTAGCTGATTTTTCGATAGCAGGTGAAGCTGTGAAGAAAGAAAGCG 1310
```

RESULT 7
ID AA022616 standard; DNA; 1533 BP.
XX

AC AA022616;
XX
DT 07-JUL-1992 (first entry)
XX

DE Carthamus tinctorius desaturase gene.
XX

KM Safflower; fatty acid synthesis; seed; acyl carrier protein;
XX lipids; ss.

XX

```
OS Carthamus tinctorius.  
FH Key Location/Qualifiers  
FT CDS 105..1294  
FT /*tag= a  
FT /product= desaturase  
XX  
PN W09203564-A.  
XX  
PD 05-MAR-1992.  
XX  
PE 15-AUG-1991; 91WO-U005801.  
XX  
PR 26-JUN-1991; 91US-0721761.  
PR 15-AUG-1990; 90US-0568493.  
XX  
PA (CALG-) CALGENE INC.  
PI Knauf VC, Thompson GA;  
XX  
DR WPI; 1992-096907/12.  
DR P-PDB; AAR22048.  
XX  
PT New plant beta-keto:acyl synthase protein - obtd. from Ricinus  
PT communis, useful e.g. for modifying fatty acid compns.  
XX  
PS Disclosure; Fig 8; 157Pp; English.  
XX  
CC The desaturase gene isolated from Carthamus tinctorius was present  
CC as the clone pcGN254. The clone can be used to construct: acyl  
CC carrier protein expression cassettes in a binary vector for plant  
CC transformation. This allows integration of nucleic acids encoding  
CC a desaturase sequence and a synthase sequence into the genome of a  
CC host cell. A plant desaturase includes any enzyme capable of  
CC catalysing the insertion of a first double bond into a fatty acid  
CC -ACP moiety especially between C9 and C10.  
CC See also AA022606-21.  
XX  
SQ Sequence 1533 BP; 421 A; 327 C; 391 G; 394 T; 0 other;  
XX  
Query Match 38.8%; Score 522; DB 13; Length 1533;  
Best Local Similarity 68.5%; Pred. No. 1.3e-136;  
Matches 739; Conservative 0; Mismatches 331; Indels 9; Gaps 1;  
QY 166 AACTCCATGTTCTTGAATCTCAAAAGTCCGCCAATCTTCAAGTCACTACTATG 225  
Db 241 AATGCCAAGAAAGCTTTTCAACCTCCACGAGAGTTCATGTTCAAGTGAAGCACTCATG 300  
QY 226 CCACCCCAAAAGCTAGAAATATTCAGTCCCTTGATGATTTGGCTAGAACATATGTTG 285  
Db 301 CCACCCCAAAAGATGAGATATTCAAATCCATCGAGGTTGGCTGAGCAGAACATATTTG 360  
QY 286 ATTCACCTCAATCTGTCGAGAAATCTTGGCAACCAAGACTCTTGGCGGATCCGGTG 345  
Db 361 GTTCACCTTAAAGCCAGTGGAGAAATGTTGGCAACACAGGATTTTGGCCGAGCTTGCA 420  
QY 346 TCAAGACGATTCGAGCAAGTCCGGAGTTGAGGAGAAAGGCGCAAGAGATTCGCCGA 405  
Db 421 TCTGAAGATTTGATGAACAAGTCAAGAACTAAGGGCAAGAGCAAGAGATTCCTGAT 480  
QY 406 GACTATTTTGTGTTAGTGTGAGATATGATCACAAGAGAGACTTCCAACTATATG 465  
Db 481 GATTACTTTGTGTTGTGGAGATATGATTAACAGAGAAAGCCCTACTACTTACCAA 540  
QY 466 TCTATGCTCAATAGTGTGATTAAGAGATGAGAGTGGAGTGGAGTGGAGTGGAGTGGAG 525  
Db 541 ACAATGCTTAATACCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
QY 526 GCAATGTGACTAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 585  
Db 601 GCTGTGTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 660  
QY 586 TACCTTATTTGTCGGAAGGTTGATATAGCAAGAAATTTGAGAAAGATTAATTCATATCTC 645
```

Db 661 TATCTTACCTTTTGGGGGGGTAGACATGAGGAGATACAGAAACAAATTCAGTATCTC 720
QY 646 ATCGGCTCAGGAATGATATATCAAGTCAAGAAACAGCCCCCTACTAGGCTTCAATACACA 705
Db 721 ATTGGGTCAGGAATGATATCTTCCGTAACGAAACAGCCCCCTACTAGGCTTCAATACACA 780
QY 706 TCTCTTCCAGAGAGACACCTTCAATATCCATGCCACACAGCCCAACCTGGCCCAACAC 765
Db 781 TCGTTTCAAGAGCGCTGACATTTGTCTCAGGAAACACCGCAGCATGCAAGAGAT 840
QY 766 TACGGCGCAAGAACCTCCGTCACATCGGGGCTCCACATCGGCTCCGAGAGAAAGCGCAC 825
Db 841 CATGGGACGTGAACTGGCCAAATTTGTGTACAAATCGGCTGTGAGAAACCGCTCAC 900
QY 826 GCCACAGCTACACCAAGATCGTGGAAAGCTCGCTGAGATCGAACCCCGACACACAGTA 885
Db 901 GAGACCGCTTATACAAAGATATGCGAAAGCATATTCGAGATCGATCCGATGCGACCGTT 960
QY 886 ATTGCTTTTGCAGATATGATGCGCAAAAAATAACAATGCCAGCCACTTGATGTAGCAC 945
Db 961 CTTCCTTTTGGCCAGATGATGAGAAAGATCTCGATGCCCGCACACTTGATGTAGCAT 1020
QY 946 GGAAGTACGCAACTCTTTTAAACATTTGACGGCGGTGCTCAGAGAGTNGGCTTTAT 1005
Db 1021 GGGCGTATGACAACTCTTGAACATTTCTCGGGGTGTGCCCAAAAGACTCGGCTCAC 1080
QY 1006 TCTGCGTTGGATTATGTCGACATCTTATAGATTTCTGTGATTAATGAAATGTGAAGAAG 1065
Db 1081 ACCGCCAAAGACTACGCCGACATCTGGAATTTCTGCGGGCGGTGGAAGTGGCGGAT 1140
QY 1066 CTTAAGGGGCTGTGCGACGAGGGCCGAAAGCCGAGAAATATGTGTGAATTTGGTCCC 1125
Db 1141 TTGACCGGCTATCTGTGTGAAGGCGCTTAAAGCGCAAGATTATGTTTGGGTTGCCACA 1200
QY 1126 AAGATTAGCGAGTGAAGAGAAAGTGCAGGGAGGAGAGAAAGAGAAAGTGCAGCAC 1185
Db 1201 AGATCAGAGAGGCTGAGGAGAGAGCTCAAGGGCGAGCAAG-----GAAGGACT 1251
QY 1186 CCTGTTTCTTTCACTGAGTATTTCAATCGGAGTTGAAGATATGACAGAGAGGGAAG 1244
Db 1252 GTTGTTCATTCAGCTGATTTTCGATATGACAGGTGAAGCTGTGAACAAAAAAGCG 1310
RESULT 8
AA064003
ID AA064003 standard; cDNA; 1533 BP.
AC AA064003;
XX
DT 01-DEC-1994 (first entry)
XX
DE Sequence encoding desaturase enzyme.
XX
KW Synthesase; plants; oil; seed; fatty acids; gene expression;
KM biosynthesis; ss.
XX
OS C. tinctorius.
XX
FH Key Location/Qualifiers
FT CDS 106..1296
FT /tag= a
FT /product= Desaturase.
FT sig_peptide 106..211
FT /tag= b
FT mat_peptide 212..1296
FT /*tag= c
XX
PN W09410189-A.
XX
PD 11-MAY-1994.
XX
PF 02-NOV-1993; 93MO-US10526.

XX
PR 02-NOV-1992; 92US-0971182.
XX
XX (CALJ) CALGENE INC.
PA
XX
PI Knaufl VC, Thompson GA;
DR WPI: 1994-167378/20.
DR P-PSDB: AAR54033.
XX
PT DNA constructs encoding beta-(keto:acyl)-ACP synthase - useful to
PT modify the oil content of seeds, e.g. for dietary purposes
XX
XX Disclosure; Figure 10; 85pp; English.
XX
CC Higher plants appear to share a common metabolic pathway for the
CC synthesis of fatty acids. Genes encoding synthase proteins may be
CC used in nucleic acid constructs to modulate the amount of synthase
CC activity in a host cell. Nucleic acid constructs may also be
CC designed to decrease the expression of a synthase protein, i.e.,
CC constructs containing anti-sense synthase sequences. The constructs
CC allow the generation of plants bearing seeds which have enhanced oil
CC yields and/or altered compositions of oils. The production of
CC common plant unsaturated fatty acids is catalysed by a desaturase.
CC Oleic, linoleic and alpha-linoleic acids found in storage
CC triglycerides are produced from the desaturation of stearoyl-ACP to
CC form Oleoyl-ACP.
SQ Sequence 1533 BP; 420 A; 327 C; 392 G; 394 T; 0 other;
Query Match 38.8%; Score 522; DB 15; Length 1533;
Best Local Similarity 68.5%; Pred. No. 1,3e-136;
Matches 739; Conservative 0; Mismatches 331; Indels 9; Gaps 1;
QY 166 AACTCCATGGTCTTCTGTAATCTCAAAAGTCCGCAATCTTCAAGTCACTCACTATG 225
Db 241 AATGCCAAGAAAGCTTTTCAACCTCCACGAGAGGTTCTATGAGTGACGCACTCCATG 300
QY 226 CCACCCCAAAAGCTAGAAATATTCAGTCCCTGATGATGGGCTGAGAACATTTGTTG 285
Db 301 CCACACAGAAAGATAGAGATTTTCAATCCATGAGGCTTGGCTGACGACAAATATTTG 360
QY 286 ATTACCTCAAAATCTGTGCAAGAAATCTTGGCAACACAGACTACTTCCGGATCCGGTG 345
Db 361 GTTCACCTAAAGCCAGTGGAGAAATGTTGGCAAGACAGAGATTTCTTGGCGACCTCGCA 420
QY 346 TCAAGCGGATTCAGAGAGCAAGTCCGGAAGTTAGGGAAGGCCAAGAGATTTCCGAC 405
Db 421 TCTGAAGGATTTGATCAACCAAGTCAAGGAACTAAGGCAAGAGAGGATTTCCGTAT 480
QY 406 GACTATTTTGTGTTTACTTGTGAGATATGATCAGAGAAAGCAACCTCCACATATATG 465
Db 481 GATTACTTCTTTTGTGTTGTTGATATGATATATACAGAGAAACCTTACTTACTTCCAA 540
QY 466 TCTATGCTCAATAGTGTGTGATGATTAAGATGAGACTGGGGCTGAGCCGACGCTTGG 525
Db 541 ACAATGCTTAATACCTAGATGTTGATGATGAGACTGGGGCTTACGCTTACGCTTGG 600
QY 526 GCAATGTGACTAGGGCATGAGACTGCCGAAGAGATATGATGATACCTTCTCAATTAAG 585
Db 601 GCTGTCTGAGATGAGGCTTGACAGCTGAAGAAACAGGCAATGCGCATCTCCACACC 660
QY 586 TACCTTATTTTGTGGAAGGGTTGATATGAGGAAATGAGAGACCTTTCATATCTTC 645
Db 661 TATCTTACCTTTTCTGGGGGTGAGCATGAGGCAATATCAGAGACAAATTAATATCTTC 720
QY 646 ATCGGCTCAGGAATGATATCAAGAAACAGCCCCCTACTAGGCTTCAATACACA 705
Db 721 ATTGGGTCAGGAATGATATCTTCCGTAACGAAACAGCCCCCTACTAGGCTTCAATACACA 780
QY 706 TCTCTTCCAGAGAGACACCTTCAATATCCATGCCACACAGCCCAACCTGGCCCAACAC 765
Db 781 TCGTTTCAAGAGCGTGCACATTTGTCTCAGCGGAAACACCGCAGCATGCAAGAGAT 840

QY	766	TATGGGACAAAGAACCTCCGCTACATCTCCGCTCATCGGCTCCGAGAGAAAGCGCAC	825
Db	841	CATGGGACGTGAACACTGGCGCAAAATTTTGGTGACATGGCTGTGACAAAAGGGTAC	900
QY	826	GCCACACCCCTACACCAAGATCGTGGAAAAGCTCGAGATGACGCCCGACACACAGTA	885
Db	901	GAGACGCCCTATATCAAAAGATAGTCGAAAAGCTATTTCGAATGTGATCTGTATGGCACGTT	960
QY	886	ATTGCTTTTGCAGATATGATGCGCCAAAAAAATPACATGCCAGCGCACTTGATTAGAC	945
Db	961	CTTCTCTTTTCCCGACATGATGAGAAAAAAGATCTCGATCCCGCACACTTGATGACAT	1020
QY	946	GGAGTACACGAACCTCTTTTAAACAATTCACGGGCGTTGTCAGAGATGAGGTTAT	1005
Db	1021	GGGCGTATGACAACTCTTTCGACATTTCTGCGCGTTGCCCAAAAGACTCGGCGCTTAC	1086
QY	1006	TCTGCGTGGATTATTTCGCACATCTTAGATTTCTGTGGATTAATGGAATGTGAAAG	1065
Db	1081	ACCCCAAAAGACTACGCCGACATCTGGAATTTCTGTGGCGGGTGGAAATGTGCGAT	1148
QY	1066	CTTACGGGGCTTTCGACAGAGGGGCCAAAAAGCGCAGGAATATGTGTGAATTTGGGTCCC	1125
Db	1141	TTTGACCGGCTATCTGTGTGAAGGGCCCTAAAGCCCAAGATTATGTTTGGCGTTGCCACA	1200
QY	1126	AAGATTAGCGAGTGGAAAGAAAGTCAGAGGGGAGAGAGAAAGAAAGACTGACAC	1185
Db	1201	AGATATCAAGAGCGTGGAGAGAGAACTCAAGGCGAGCAAA-----GAAAGACT	1251
QY	1186	CTGTGTTCTTTCACGTGATTTTCAATTCGGAGTTGAAGATATGAACAGAGAAGGAGG	1244
Db	1252	GTGTTCCATCTACCTGATTTTTCGATAGACAGTGAACCTGTGAAGAAAAAAAAGG	1310

XX	AAV15250	standard; cDNA to mRNA; 1533 BP.
XX	AAV15250;	
XX	AAV15250;	
DT	28-MAY-1998	(first entry)
XX	Carthamus tinctorius desaturase from cDNA clone pCGN2754.	
XX	Carthamus tinctorius; safflower; delta-9 desaturase; oilseed;	
KW	fatty acid saturation; ds.	
XX		
OS	Carthamus tinctorius.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	106..1296
FT		/*tag= a
FT		/product= "desaturase"
FT	sig_peptide	106..204
FT		/*tag= b
FT	mat_peptide	205..1293
FT		/*tag= c
XX		
PN	US5723595-A.	
XX		
PD	03-MAR-1998.	
XX		
PF	06-JUN-1995;	95US-0471791.
XX		
PR	16-SEP-1991;	91US-0762762.
PR	16-MAR-1990;	90US-0494106.
PR	13-AUG-1990;	90US-0567373.
PR	14-NOV-1990;	90US-0615784.
PR	14-MAR-1991;	91MO-US01746.
PR	06-JUN-1995;	95US-0471791.
XX		
PA	(CALJ) CALGENE INC.	
XX		

PI Knauf VC; Thompson GA;
XX
XX WPI: 1998-178544/16.
DR P-PSDB: AAW44349.
XX
PT DNA encoding plant delta-9 desaturase protein - having amino acid
PR sequence of *Carthamus tinctorius* desaturase, useful for, e.g.,
PT producing oil-seeds with modified levels of fatty acid saturation
XX
XX
PS Example 5: Column 51-54; 87pp; English.

XX
CC The present sequence encodes a *Carthamus tinctorius* desaturase from
CC clone pCGM2754. The present invention describes a recombinant DNA
CC construct comprising a DNA sequence encoding a plant Delta-9-desaturase
CC protein. The present invention also provides a method of modifying fatty
CC acid composition in a host plant cell from a given fatty acid saturation
CC level to a different fatty acid saturation, comprising growing a host plant
CC cell containing a recombinant DNA sequence which encodes a plant
CC desaturase under the control of regulatory elements functional in the
CC plant cell during lipid accumulation. Also, oilseeds having a modified
CC level of fatty acid saturation and oils produced from such oilseeds.
XX
SQ Sequence 1533 BP; 420 A; 327 C; 392 G; 394 T; 0 other;

	Query Match	38.8%	Score 522	DB 19	Length 1533	
	Best Local Similarity	68.5%	Pred. No. 1.3e-116			
	Matches 739	Conservative 0	Mismatches 331	Indels 9	Gaps 1	
QY	166	AACCTCATGGTCTCTGATATATCTCAAAGATCCCAAAATCTTCAAGTCACATCACTCTATG	225			
DB	241	AATGCCAAGAACCCCTTTTCAACCTCCAGAGAGGTTCATGTTCAAGTCAGCAGCATCCATG	300			
QY	226	CCACCCCAAAGACTTGAAATATTCAAGTCCCTGATGATTTGGGCTAGACAATGTGTTG	285			
DB	301	CCACCAAGAGAGATGAGATTTTCAAAATCCATCGAGGGGTGGGCTGAGACAGACATATTG	360			
QY	286	ATTCACTCAATATCTGTGGAGAAATCTTGGCAACCAAGAACTACTTCCGGATCCGGTGG	345			
DB	361	GTTCACCTTAAGCCAGTGGAGAAATGTTGGCAAGCAAGATTTCTTCCGGACCTTCA	420			
QY	346	TCAGACGAGATTCGAGAGACCAAGTCGGGAGTTGAGGCAAGAGGCCCAAGAGATTTCCGAC	405			
DB	421	TCTGAGAGATTTGATGAAACAAGTCAAGGAACTAAGGGCAAGGCAAGCAAGAGATTTCTAT	480			
QY	406	GACTATTTTGTGGTTAGTTAGTAGATATGATCACAGAAAGACACTTCCAATATATG	465			
DB	481	GATTACTTTGTTGTTGGTTGGATATGATATACAGAGAAAGCCCTACACTTACCA	540			
QY	466	TCTATGCTCAATAGTGTGATGTCTTTAAGATGAGACTGGGGCTGAGCCCATGCTTTGG	525			
DB	541	ACAATGCTTAATATACCTCTGATGTGTACGTGTAGAGCTGGGGGCTTACGGCTTAC	600			
QY	526	GCAATGTGAGTACAGGCAATGAGCTCCGAAAGAAATGACATGGTACCTTCTCAATAG	585			
DB	601	GCTGTCTGAGCTAGGGCTTGGACACCTGAGAAAGACAGCATGGGAGTCTTCCACACC	660			
QY	586	TACCTTTATTTTCTCGAAGGGTTATATGAGGAATATGGAAGAACTATTCATATATCTC	645			
DB	661	TATCTCTACCTTCTTGGGGGGGTAAACATGAGAGCAAGATACAGAAACAATTCAGTATCTC	720			
QY	646	ATCGGCTCAGGAATGATATCAAGTCAAGAAAACAGCCCTACTAGGCTCATCTACACA	705			
DB	721	ATTGGTACAGGAATGATCTCTGTACCGAAAACAGCCCTACTAGGCTCATCTACACA	780			
QY	706	TCCCTTCCAAGAGAGCAACTTCTATATCCATATGCCAACACACAGCCAACTGGCCCAACAC	765			
DB	781	TGCTTTCAAGACCTGCCACATTTTCTCTCAGGAAACACCGCCAGGCATGCAAAAGAT	840			
QY	766	TACGGCTCAAGAACCTCGCTCACATCTGCGGCTCCATTCGGCTCCGAGAGAGCGCAC	825			
DB	841	CATGGGAGAGTGAACCTGGCCCAATTTGTGTACAAATCGGCTCTGAGAAAAGCGTAC	900			
QY	826	GCCACAGCTTACCCCAATGCTGAAAAAGCTCGCTGATGATGATCCCGACACACACTA	885			

Db	901	GAGACCGCTTATATCAAAGATAGTCGAAAAGCTATTCCAGATCGATTCTGATGCGACCGTT	960
Qy	886	ATTGCTTTTGGCAGATATGATGCGCAAAAAAATAACAATGCCAGCGCACTTGATGTACGAC	945
Db	961	CTTGCCTTTTGGCCGACATGATGAGGAAAAAAGATCTCGATGGCCCGACACTTGATGTAGCAT	1020
Qy	946	GGAGTGCAGCAACTCTTTTAAACATTTTACACGCGGTTGCTCAGACAGTGNCGGTTTAT	1005
Db	1021	GGGCGTGATGACAAACCTCTTCGAAACATTTCTCGCGGGTTGGCCCAAAAGACTGCGGCTTAC	1080
Qy	1006	CTGCGCTTGATTAATTGCGCACTCTTTGAGTTTCTGGTGATTAATGGAATGTGGAAAGG	1065
Db	1081	ACCGCCAAAGACTATACGCCGACATACTCGAAATTTCTGGTTCGGCGGTGGAATGTGCGGAT	1140
Qy	1066	CTTACGGGGGCTGTGCGACGAGGGCGCGAAAAAGCGCAGAGAAATATGTTGTAATGGGTTCCC	1125
Db	1141	TTGACCGCGCTATCTGGTGAAGGGCGTAAAGCGCAAGATTATGTTCCGGTTTCCACCA	1200
Qy	1126	AGATTAAGCGAGTGCAGAGAAAGTGCAGGGCAGAGAGAAGAAAGAAAGCTGAGCAC	1185
Db	1201	AGATTCAGAAAGCGCTGGGAGGAGACGTCAAGGGCGAGCAAAAG-----GAAGGACTT	1251
Qy	1186	CCGCTTCTTTCAGCTGGAATTTCCATCGGGAGTGAAGATGACAGAGGAAGG	1244
Db	1252	GTTGTTCCATTTCAGCTGGATTTTCGATAGACAGGTGAAGCTGTGAAGAAAAAAAACG	1310
RESULT 10			
AAx35666			
ID	AAx35666 standard; DNA; 1533 BP.		
XX	AAx35666;		
XX	AAx35666;		
DT	16-JUL-1999 (first entry)		
XX	DNA encoding a stearyl-acyl carrier protein desaturase.		
XX	Localised mutation; target gene; plant cell;		
KM	recombinogenic oligonucleobase; selective growth advantage;		
KM	herbicide resistance; preservation; fruit; flower; ss.		
XX	Carthamus tinctorius.		
OS	Carthamus tinctorius.		
PN	WO9907865-A1.		
PD	18-FEB-1999.		
PE	05-AUG-1998: 98WO-US16267.		
PR	05-AUG-1997: 97US-0054836.		
XX	(KIME-) KIMERAGEN INC.		
PI	Arntzen CJ, Kipp PB, Kumar R, May GD;		
XX	WPI: 1999-302251/25.		
DR	Introducing mutations into target genes in plant cells - using a		
XX	recombinogenic oligonucleobase comprising 2 regions homologous to a		
PI	target gene and an intervening mutant region		
XX	Example 5; Page 40-41; 53pp; English.		
PS	The specification describes methods for introducing localized mutations		
CC	into target genes in plant cells. The methods comprise using a		
CC	recombinogenic oligonucleobase comprising 2 regions homologous to a		
CC	target gene and an intervening mutant region. The methods can be used		
CC	to introduce localized mutations into target genes to introduce desirable		
CC	traits, e.g. selective growth advantage under appropriate selective		
CC	conditions, change in colour of plant cells growing in a callus,		
CC	herbicide resistance, or improved preservation of fruit or flowers.		
CC	They can be used in plants such as maize, wheat, rice, lettuce, potato,		

[illegible]


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RESULT 12
AA063437
ID AA063437 standard; cDNA; 1529 BP.
XX
XX AA063437;
AC
XX
XX 03-JUL-1997 (first entry)
DT
XX
XX
DE Raped seed stearyl-ACP desaturase cDNA clone BND11.
XX
XX Stearyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;
KM stearic acid; transgenic plant; oilseed;
XX vegetable oil; mangosteen; Garcinia mangifera; ss.
OS Brassica napus cv. 212/86.
XX
XX
FH Key Location/Qualifiers
FT CDS 25..1230
FT /tag= a
XX
XX WO9712047-A1.
XX
XX 03-APR-1997.
XX
XX
XX 30-SEP-1996; 96WO-US16078.
XX
XX
XX 29-SEP-1995; 95US-0537083.
XX
XX (CALJ ) CALGENE INC.
XX
XX
XX Knauf VC, Kridl J, Lassner MW;
XX
XX WPI; 1997-212906/19.
XX
XX P-PSDB; AAM14797.
XX
XX
XX Increasing levels of stearate in plant seed triglyceride(s)
XX using a DNA sequence encoding acyl-ACP thioesterase protein having
XX substantial activity on C18:0 acyl-ACP substrates
XX
XX
XX Example 5; F196A-6C; 55pp; English.
XX
XX
XX A cDNA clone (AA063437), designated BND11, codes for oilseed rape
XX stearyl-ACP desaturase (AAM14797), an enzyme that catalyzes the
XX desaturation of stearyl-ACP (C18:0) to oleoyl-ACP (C18:1). BND11
XX and clone BND9 (see also AA063438) were isolated from a cDNA library
XX constructed from RNA obtd. from mid maturation seeds of Brassica
XX napus cv. 212/86. The library was screened with the coding region
XX of a delta-9 desaturase gene from Brassica campestris. An antisense
XX gene was constructed to generate antisense RNA homologous to both
XX BND9 and BND11. In transgenic Brassica plants expressing the
XX stearyl-ACP desaturase antisense construct and mangosteen Class I
XX acyl-ACP thioesterase gammaPATAI (see also AAM14795), levels of C18:0
XX in the seed oil may exceed 50% of total fatty acids.
XX
XX
XX Sequence 1529 BP; 414 A; 351 C; 363 G; 401 T; 0 other;
SQ
Query Match 38.8%; Score 521.4; DB 18; Length 1529;
Best Local Similarity 71.3%; Pred. No. 1.9e-136;
Matches 687; Conservative 0; Mismatches 277; Indels 0; Gaps 0;
OY 206 TTCAGTCACTGACTCTATGACCCCAAGAGCTAGAATATATTCAGTCCCTTGATGATT 265
DB 215 TTCAGTCTGCTGATCCATGCCACCCCAAGATGCAATCTTCAATCTGATGAGAGACT 274
OY 266 GGGCTAGGACAATGTGTTGATTCACCTCAATCTGTCGAGAAATCTGCAACCAACAG 325
DB 275 GGGCCGAGACAACCTCTACCTCAACCTCAAGAGCTGAGAAAGTATGAGCAGCCAG 334
OY 326 ACTACTTGGCCGATCCGGGTGACAGAGGATTCGAGAGCAAGTCCGGAGTTAGGAGAA 385
DB 335 ACTCTTACCGGACCTGCTCTCCGAGGGGTGCAAGAGCAGTAAGAAAGATTAAAGAGAA 394
FH Db
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OY 386 GGGCCAAAGAGATTCCCGAGACTATTGTTGGTGTAGTTGAGATATATCAGAGAG 445
DB 395 GAGCAAGAGAGCTCCCGAGATGATTAATCTGTTGTTGGTGGAGATGATACAGAG 454
OY 446 AAGCACTTCCAAATATATGCTATGCTCAATGATGATGATGATTAAGATGAGACTG 505
DB 455 AAGGCTTCCCACTTCAACCAATGCTGAACACTTGGATGGTGAAGGATGAGACTG 514
OY 506 GGGCTGAGCCAGTGTCTGGGCAATGTGAGCTAGGCGATGAGCTCCGAGAGAGTGA 565
DB 515 GTGCTAGCCCACTTCAATGAGGCGGTTTGAGACTGAGGCTTGAGCTGCTGAGAGAG 574
OY 566 ATGCTGACCTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 625
DB 575 ACGGTGATCTTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 634
OY 626 AGAAGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 685
DB 635 AGAAGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 694
OY 686 ACCTAGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 745
DB 695 ACCTTGGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 754
OY 746 CAGCCAAAGCTGGCCCAACACTACGCGGACAAGAACTGCTCAATCTGCGCTCCAT 805
DB 755 CAGCTGGCCCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 814
OY 806 CTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 865
DB 815 CTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 874
OY 866 TTCAGCCCGACACACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 925
DB 875 TTGATCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 934
OY 926 CAGCGCACTTGTATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 985
DB 935 CTGCTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 994
OY 986 CTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1045
DB 995 CTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1054
OY 1046 ATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1105
DB 1055 GAGAGTGAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1114
OY 1106 ATGCTGTGAATTTGGTCCCAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1165
DB 1115 ATGATGTTGGGTGACCTCCAGAAATCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1174
OY 1166 AGAA 1169
DB 1175 AGAA 1178
FH Db
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RESULT 13
AA020187
ID AA020187 standard; cDNA to mRNA; 2243 BP.
XX
XX AA020187;
AC
XX
XX 31-MAR-1992 (first entry)
DT
XX
XX Soybean seed stearyl-ACP desaturase coding sequence from pds1.
DE
XX
XX soya bean; plant oil; stearic acid; ss.
KM
XX
XX Glycine max strain Cultivar Wye.
OS
XX
XX
FH Key Location/Qualifiers
```

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FT      5'UTR      1..69
FT      /tag= a
FT      transil_peptide 70..165
FT      /tag= b
FT      /note= "putative"
FT      mat_peptide 166..1242
FT      /tag= c
FT      3'UTR      1246..2243
FT      /tag= d
XX      MO9118985-A.
XX      12-DEC-1991.
XX      16-MAY-1991; 91MO-US03288.
XX      25-MAY-1990; 90US-0529049.
XX      (DUPO ) DU PONT DE NEMOURS CO.
XX      Hitz WD, Yadav N;
XX      WPI; 1992-007469/01.
XX      P-PSDB; AAR20011.
XX      DNA encoding soybean stearyl-ACP desaturase enzyme and precursor
XX      - and chimeric genes, for plant transformation and control of
XX      PT levels of satd. and unsaturated fatty acids in edible oils
XX      PS Claim 1; Page 54; 70pp; English.
XX      A Lambda ZAP cDNA library was prepared from soybean embryos polyA RNA
XX      and used to infect E.coli B84 cells. The cells were plated and
XX      CC transfected to nitrocellulose filters for hybridisation. Probes were
XX      CC designed based on the N-terminal amino acid sequence of purified
XX      CC stearyl-ACP desaturase. Six positive plaques were subjected to
XX      CC plaque purification and the regions of each vector comprising the
XX      CC cDNA inserts were excised. The resulting phagemids were used to
XX      CC infect E.coli XL-1 Blue cells to give 6 double-stranded plasmids
XX      CC pDS1 to pDS6. There was a common 0.7kb BglII fragment found in the
XX      CC desaturase gene of all 6 plasmids. The invention covers chimeric
XX      CC genes comprising nucleotides 1-2243, 70-1245 or 166-1245 of this
XX      CC sequence, linked to suitable control sequences. They are used for
XX      CC transforming oil-producing plant cells to produce antisense inhibition
XX      CC of desaturase in the seed, overexpress precursor desaturase in the
XX      CC cell plastid or express mature enzyme, respectively.
XX      CC See also AAQ20188-Q20190 and AAR20012.
XX      SQ Sequence 2243 BP; 625 A; 447 C; 528 G; 643 T; 0 other;
XX
Query Match 38.8%; Score 521.2; DB 13; Length 2243;
Best Local Similarity 68.5%; Pred. No. 2,6e-136;
Matches 743; Conservative 0; Mismatches 324; Indels 18; Gaps 1;
OY 112 CCAGTGACCAAGTACGCTCTCCAGAGGCTTTCATGCGCTTCACATCTCACTCACTCC 171
DB 118 CAAATGCCAGGCTCCGATCTCCGCTCCGATGCTCCACCCCTCCGCTCCGCTCC 177
OY 172 ATGCTTCTGATTAATCTCAAAAGTCCGCCA-----ATCTTCAAGTC 213
DB 178 AAGAGGTTGAAATATTTAGAGCCATTCCTCCAGAGAACTGCATGTTCAAGTA 237
OY 214 ACTCACTATATGACCCCAAAAGCTAGAAATATTCACGCTCCCTGATGTTGGCTAGG 273
DB 238 ACCCACTATGCTCCCGCAGAAATTTGAGATTTTCAATCTTTGGAGATTTGGCTGAC 297
OY 274 AACATGCTGTTATTCACCAATCTGTCGAGAAATCTTGGCAACACAGACTACTTG 333
DB 298 CAGAACATCTTACCTCACTCACTTAACTGTAGAAATATTTGGCAACACAGACTTTTAA 357
OY 334 CCGGATCCGCTGTCAGAGCAAGTTCGAGAGCGGAGTTCGGGAGGGAAGAGCGCAG 393
DB 358 CCGGACCCCTCTCTCAGATGATTTTGAAGCAAGTGAAGGAAGTGAAGAGAGCAAG 417

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OY 394 GAGATTCGCCGACGACATATTTTGTGCTTACGTTGAGATATGATTCACAGAGACACTT 453
DB 418 GAGATTCGAGATGATTAATTTGTTCTTGTGCGAGACATGATTCACAGAGAGGCTCTG 477
OY 454 CCACATATATGCTATGCTCAATAGTGTGATGATTAATAGATATGAGTGGGCTGAG 513
DB 478 CTTACCTACCAACATATGTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 537
OY 514 CCGAGTGTGGGCAATGAGTACGAGTACGAGTACGAGTACGAGTACGAGTACGAGTAC 573
DB 538 CTTACTTCTGCGCAATTTGGACAAAGGCAATGAGTACGAGTACGAGTACGAGTACG 597
OY 574 CTTCTCAATTAAGTACCTTATTTTGTCTGGAAGGCTTGAATGAGAAATTTGAGAACT 633
DB 598 CTTCTTAACAAATATCTGATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 657
OY 634 ATTCAATATCTCATGCGCTCAGCAATGATATCAAGTACAGAAACGCCCTACCTAGGC 693
DB 658 ATTCAATATCTCATGCGCTCAGCAATGATATCAAGTACAGAAACGCCCTACCTAGGC 717
OY 694 TTGATCTACACATCTCTCCAGAGAGAGCAACCTTCATATCCATGCAACACAGCCAG 753
DB 718 TTGATTTACACTTCACTTCAAGAGAGGCAACCTTCATATCCATGCAACACAGCCAG 777
OY 754 CTGGCCCAACACTACGCGCAAGAACCTGCTACATCTGCGCTCCATCGCTCCGAC 813
DB 778 CTTGCGAAGAGAGATGTTGACATAAATTGGCACAGATCTGCGGCAATGCTCTCAGAT 837
OY 814 GAGAACGCCGACGACCAAGCTTACACCAAGATCTGGAAGAAAGCTCCGAGATGACCC 873
DB 838 GAGAACGCCGACGACCAAGCTTACACCAAGATCTGGAAGAAAGCTCCGAGATGACCC 897
OY 874 GACACACAGATTAATCTTTCAGATATGATGATGATGATGATGATGATGATGATGAT 933
DB 898 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 957
OY 934 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 993
DB 958 CTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
OY 994 GTGNGGCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1053
DB 1018 ATTTGGGCTTACCTCAAAAGTACATGCTGATCTGATCTGATCTGATCTGATCTG 1077
OY 1054 AATGTGAAAGGCTTACGCGGCTGTGAGCAGAGGCGCAAAAGCGAGCAATATGTGTG 1113
DB 1078 AAGGTGAGCAGCTTAACGCACTTTCAGTGTGAGGGAAGAAAGGCTCAGCAATAC 1137
OY 1114 GAATGGGTCCCAAGATTTAGCGAGTGAAGAGAAAGTGCAGGCGGAAGAGAAAG 1173
DB 1138 GGGCTGCCACCAAGATTCAGAAAGTTGAGAGAGAGAGCTCAACAGAGGCAAGAGT 1197
OY 1174 AAGGC 1178
DB 1198 TCAAC 1202

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RESULT 14
AAV29236
ID AAV29236 standard; cDNA to mRNA; 2243 BP.
XX
XX AAV29236;
XX
XX 21-AUG-1998 (first entry)
XX
XX Nucleotide sequence of the soybean seed stearyl-ACP desaturase.
DE Soybean stearyl ACP-desaturase gene; chimeric gene; antisense;
KW transformation; saturated fatty acid; unsaturated fatty acid;
KW soybean oil; inhibition; polyunsaturated; monosaturated; ss.
XX
OS Glycine max.

```

```
XX Key Location/Qualifiers
FH 5 UTR 1..69
FT /*tag= a
FT CDS 70..1245
FT /*tag= b
FT /product= "soybean seed stearyl-ACP desaturase"
FT transit_peptide 70..165
FT /*tag= c
FT mat_peptide 166..1245
FT /*tag= d
FT 3'UTR 1246..2243
FT /*tag= e
XX US5760206-A.
XX 02-JUN-1998.
XX 07-JUN-1995; 95US-0474587.
XX 07-JUN-1995; 95US-0474587.
PR 19-MAY-1991; 91WO-US03288.
PR 11-DEC-1992; 92US-0995657.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Hitz WD, Perez-Grau L, Yadav NS;
XX WPI: 1998-332247/29.
XX P-PSDB; AAW37939.
XX Nucleic acids encoding soybean seed stearyl-ACP desaturase enzyme -
XX are useful for the anti-sense inhibition of the enzyme in
XX transformed plant cells
XX
XX Claim 1: Column 37-40; 26pp; English.
XX
XX This is the nucleotide sequence of the soybean stearyl
XX ACP-desaturase gene, used in the method of the invention, which
XX involves the creation of chimeric genes which are used in (antisense
XX orientation) to transform plant cells. The nucleic acids are useful
XX for controlling the levels of (un)saturated fatty acids in soybean oil.
XX In transformed cells (seeds), the chimeric genes transcribe the
XX antisense RNA to the complementary mRNA for the enzyme. This results
XX in inhibition of expression of the endogenous enzyme and reduction in
XX desaturation of seed oil. This results in seed oil which is low in
XX saturates and polyunsaturates and high in monosaturates, giving an oil
XX which is healthier.
XX
XX Sequence 2243 BP; 625 A; 447 C; 528 G; 643 T; 0 other;
XX
XX Query Match 38.8%; Score 521.2; DB 19; Length 2243;
XX Best Local Similarity 68.5%; Pred. No. 2,6e-136;
XX Matches 743; Conservative 0; Mismatches 324; Indels 18; Gaps 1;
XX
XX 112 CCAGTGACGAGAGTTCCTCCAAAGGTTTTCATGCTTCACATCTCTAATCTCC 171
XX 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
XX 118 CAATAGCCGAGCTCCCGCTCCGATGCTTCACACCTCCGCTCGGTTCC 177
XX 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
XX 172 ATGCTTTCATATCTCAAAAGTCCGCCA-----ATCTTCAAGTC 213
XX 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
XX 178 AAAGAGGTTGAAATTTTAAGAGCCATTCTACTCTCCAGAGAGATGATGTTCAAGTA 237
XX 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
XX 214 ACTCACTATGCTCCCAAAAGCTAGAAATATTCAGTCCCTTGATGATGGGCTAGG 273
XX 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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XX 274 AACAAATGCTGATTCACCTCAAAATCTGCGAAGAAATTTGGCACACCAAGACTGCTTG 333
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XX 298 CAGAACATCTTGACTCATCTTAACCTGTAGAAAATGTTGGCAACACAGAGATTTTGA 357
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XX 334 CCGGATCCGCTGTACAGAGGATTCGAGGAGCAAGTCCGGAGTGGGGAAGAGGGCCAG 393
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Qy 394 GAGATTCGCGAGACTATTTTGTGTAGTTGGAGATATGATCAGAAAGCACTT 453
Db 418 GAGATTCGAGATGATTTACTTTTGTCTTGTGCGAGACATATCAGAGAGAACTCTG 477
Qy 454 CCACATATATGCTCATGCTCAATAGTGTGTATTTAGGATGAGACTGGGCTGAG 513
Db 478 CTTACTTACCAAACTATGTTAAATCTTTGATGAGTTCGTGATGAACACAGTGCACGC 537
Qy 514 CCCAGTGTCTGGGCAATGTGACCTAGGGCATGAGTCCGAGAGATGATGATGATGAG 573
Db 538 CTTACTTCTGGGCAATTTTGAAGAGGAGTGTGAGTGTGATGAGGAAATTTGAGAAG 597
Qy 574 CTTCTCAATATGATCTTATTTGCTGTGAAGAGGTTGATGAGGAAATTTGAGAAG 633
Db 598 CTTCTTAACAATATCTGTACTTGTAGTGCAGAGTTGACATGAACAAATTTGAGAAG 657
Qy 634 ATTCAATATCTGATCGGCTCAGGAATGATATCAAGTCAAGAAACAGCCCTACTAGC 693
Db 658 ATTCAATATCTGATCGGCTCAGGAATGATATCAAGTCAAGAAACAGCCCTACTAG 717
Qy 694 TTCACTTACATCTCTTCCAGAGAGAGACACCTTCAATGCTTCCATGCCACAGCAG 753
Db 718 TTCACTTACATCTCTTCCAGAGAGAGACACCTTCAATGCTTCCATGCCACAGCAG 777
Qy 754 CTGGCCCAACACTAGCGGCGCAAGAACTCGCTCACTGCTGCGGCTCCATCGCTCG 813
Db 778 CTGGCAAGAGACATGCTGATCAATTAATTTGGCAGACATCTGCGGCTGCTGAT 837
Qy 814 GAGAAAGCCGCGACGACGCTTACACCAAGATGCTGGAAGAAAGCTGCTGATGAC 873
Db 838 GAGAAAGCCGCGACGACGCTTACACCAAGATGCTGGAAGAAAGCTGCTGATGAC 897
Qy 874 GACACAACAGTAAATGCTTGTGAGATGATGCGCAAAATAACAATGACGCGCAC 933
Db 898 GATGTACAGTATGCTTGTGAGATGATGCGCAAAATAACAATGACGCGCAC 957
Qy 934 TTGATGTACGAGAGAGTACGAGAACTTCTTTTAAATTTCAAGGCGGCTGCTGAGA 993
Db 958 CTTATGTATGAGCGCGCGCGACGACACTGTTGATTAATCTCTCCGCGCGCGCC 1017
Qy 994 GTGNGGTTTATTTCTGCTGATTTTTCGACATCTTGAAGTTCGCTGCTGCTG 1053
Db 1018 ATTTGGGTTTACCTGCAAGAGACTATGCTGACATCTGCAATTTGTTGGGAGCTG 1077
Qy 1054 AATGTGAAGGCTTACGCGGCTGTGCGACGAGGCGGCAAAAGCGCAGGAAATATG 1113
Db 1078 AAGGTGAGACAGCTTACGCGACTTTCAAGTGAAGGAGGAAAGGCTCAGGATAC 1137
Qy 1114 GAATTTGGTCCCAAGATTTAGCGGAGTGAAGAGAAAGTCCAGGGGAGAGAAAG 1173
Db 1138 GGGCTTCCCAAGAAATTCAGAGGTTGAGAGAGAGCTCAAGCAGAGAGAGTGC 1197
Qy 1174 AAAAGC 1178
Db 1198 TCACAC 1202
RESULT 15
AAND2378
ID AAND2378 standard; cDNA; 1553 BP.
XX
XX AAND2378;
XX
XX 12-FEB-2002 (first entry)
XX
XX Cotton stearyl-ACP delta9-desaturase (ghsAD-1) protein cDNA.
XX Cotton; delta9-desaturase; fatty acid delta12-desaturase; palmitic acid;
XX linoleic acid; stearic acid; oleic acid; transgenic plant;
XX cotton seed oil; stearyl-ACP delta9-desaturase; SAD-1; ss.
XX
```


OS Gossypium hirsutum.
 XX
 FH Key Location/Qualifiers
 FT CDS 13..1203
 FT /*tag= a
 FT /product= "Cotton ghsad-1 protein"
 XX
 PN MO200179499-A1.
 XX
 PD 25-OCT-2001.
 XX
 PF 18-APR-2001; 2001MO-AU00436.
 XX
 PR 18-APR-2000; 2000US-198124P.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Green A, Singh S, Liu Q;
 XX
 DR WPI: 2001-602932/68.
 DR P-PSDB; AAE13419.
 XX
 PT Modifying endogenous oil of cotton plants, to produce cotton seed oil
 PT with reduced palmitic and/or linoleic acid content, involves producing
 PT transgenic plants containing a fatty acid biosynthesis gene in a
 PT construct.
 PS
 PS Claim 2: Fig 2: 201pp; English.
 XX
 CC The invention relates to a method for modifying the endogenous oil of a
 CC cotton plant, to produce cotton seed oil. The method comprises producing
 CC a transgenic cotton plant having a gene construct which includes a fatty
 CC acid biosynthesis gene operably linked to a promoter sequence capable of
 CC conferring expression of the delta9-desaturase (delta9 stearoyl-ACP
 CC desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-
 CC desaturase) gene, in the seed of a cotton plant. The invention is useful
 CC for producing cottonseed oil with reduced palmitic and/or linoleic acid
 CC content, and increased stearic and/or oleic acid content. The present
 CC sequence is cotton Stearoyl-ACP delta9-desaturase (ghsad-1) protein cDNA
 CC related to the invention.
 XX
 XX
 SQ Sequence 1553 BP; 454 A; 296 C; 370 G; 433 T; 0 other;
 Query Match 38.4%; Score 516.4; DB 22; Length 1553;
 Best Local Similarity 68.4%; Pred. No. 4.8e-135;
 Matches 737; Conservative 0; Mismatches 322; Indels 18; Gaps 1;
 QY 111 ACCAGTACAGAGTTCAGCTTCAGAGGTTTCATGCGTTCACATCTCACTTAATCTC 170
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 QY 171 CATGCTTCTGATATATCTCAAAAGTCCGCCAATC-----TTCAAGT 212
 DB 11 1 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 135 CAAGAGGTTGGGAATCTGAAAAGGCTTTCAAGCCTCCAAAGAGGTGCTGTTCAGAT 194
 DB 11 1 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 213 CACTCACTATGCAACCCCAAGAGTGAATATTTCAAGTCCCTTGATGATGGGCTAG 272
 DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 195 CACCACCTCATCCCGCTCACAAAGATTGATCTTAAATCTTTGAGGGCTGGGCTGA 254
 DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 273 GAACATGTGTTGATTCACCTCAATCTGCGAAGAAATCTTGCAACCAACACTACTT 332
 DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 255 GAACAACATTTGACTGACCTCAACACAGTTGGAATGTTGGCAACCCCGCACTTTCT 314
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 QY 333 GCCGATCCGCTGTCAGACGATTCGAGAGCAAGTGCAGGAGTTGAGGAAGGCCAA 392
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 QY 375 GGAGATCCAGATGATGATTTGATTTGTTGATGATGATGATGATGATGATGATGAT 434
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 QY 453 TCCAACTATATGCTCATAGGTGATGATTAAGATGAGAGTGGGCTGA 512
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 QY 513 GCCAGTCTTGGGCAATGTGACATAGGCGATGAGACTGCCGAAGAGAAATAGATGCTGA 572
 DB 1 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 495 CTTTACCCCTTGGGCCATTTTGAACAGGCGTTGAGACTGCTGAGAAACAGAGCATGCTGA 554
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 QY 555 TCTGCTTAATTAAGATCTTACTTGTGCGAGAGTGTGACATGAGCAATTTGAGAGAC 614
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 QY 615 AATCAGTACTTGAATGATGAGATGATCTCTATACAGATGATGATGATGATGATGATG 674
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 QY 693 CTTTCACTACACATCTTCCAGAGAGACACCTTCATATCCCATGCCAACACAGCCAA 752
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 QY 675 ATTCAATATATCTTCTGTCAGAAAGGCACTTTATTTCCCATGGAATACAGGCAG 734
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 QY 753 GCTGGCCCAACACTACGCGCAAGAAGCTGCTACATCTGCGGCTCCATGCTCGA 812
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 QY 855 TGATGAACAGTCTCTGCAATTTGCTGATGATGATGATGATGATGATGATGATGATG 914
 DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 933 CTTGATGATGACGAGGAGTACGAACTTTTAAACATTTACGCGGCTGCTGAGAG 992
 DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 915 GTTCATCTATGATGAGGAGATATTAATCTTATTTGACCACTACTACCTGTTCCCAAG 974
 DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 QY 993 AGTNGGCTTATTTGCGGTTGATTTGATTTGAGCATCTTGAAGTTGCTGATGATGATG 1052
 DB 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
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 Job time : 311 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 21:12:16 ; Search time 3483 Seconds

(without alignments)
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Title: US-09-732-597-1

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	613.4	45.6	1297	6	A74271	A74271 Sequence 1
2	613.4	45.6	1309	8	COVACIACI	I12944 Sequence 1
3	613.4	45.6	1309	8	COVACIACI	M93115 Coriander
4	573.8	42.7	1643	8	RCCSACPD	M59857 Ricinus com
5	572	42.6	1662	8	RCCSACPD	X56508 R. communis
6	572	42.6	1668	6	I90191	I90191 Sequence 1
7	564.4	42.0	1580	8	SSMSACPD	D42086 Sesame mRNA
8	550	40.9	1194	8	SIN31331	AJ313331 Sesamum 1
9	537.4	40.0	1407	8	CUSACPD	M59858 Cucumis sat
10	533	39.7	1509	8	AF051134	AF051134 Macfadysen
11	526.8	39.2	1319	8	TA007552	U07552 Thunbergia
12	524	39.0	1576	8	SMMSACPD	M83199 Stimonidia
13	523.8	39.0	1548	8	AF172728	AF172728 Arachis h
14	522	38.8	1533	6	I16556	I16556 Sequence 32
15	522	38.8	1533	6	I19664	I19664 Sequence 32
16	522	38.8	1533	6	I90189	I90189 Sequence 12
17	522	38.8	1533	6	CAMSACPD	M61109 C. lincetoru
18	521.2	38.8	1546	6	A74273	I13990 Sequence 1
19	520	38.7	1524	6	A74273	A74273 Sequence 3
20	520	38.7	1524	8	BNSACPD	X63364 B. napus mRN
21	515.4	38.3	1517	8	AF116861	AF116861 Persica am
22	514.2	38.3	1447	8	LUSACPD	X70862 L. usitatiss
23	513.2	38.2	1206	8	AF395441	AF395441 Arabidops
24	513	38.2	1621	6	AR195536	AR195536 Sequence
25	512.6	38.1	1557	8	GHSACPD	X95988 G. hirsutum
26	511.8	38.1	1495	6	I90194	I90194 Sequence 19
27	511.8	38.1	1495	6	BRSACPD	X60978 B. rapa cv. R
28	511.6	38.1	1206	8	AY094014	AY094014 Arabidops
29	511.6	38.1	1623	8	SOVSACPD	L34346 Glycine max
30	511.6	38.1	1711	8	AY048233	AY048233 Arabidops
31	508.2	37.8	1516	8	BNAACPD	X97325 B. napus mRN
32	506.6	37.7	1622	8	ATSPACPD	X93461 A. thaliana
33	506.4	37.7	1768	8	SCSACPD	X78835 S. commerson
34	500.4	37.2	1653	8	AY056428	AY056428 Arabidops
35	499.8	37.2	1185	8	AY090324	AY090324 Arabidops
36	499.6	37.2	1493	8	OE058141	U58141 Olea europae
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42	493.2	36.7	1335	8	HAU91339	U91339 Helianthus
43	493.2	36.7	1507	8	POTSACPD	M91338 Solanum tub
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45	489.2	36.4	1191	8	HAN242632	AJ242632 Helianthu

ALIGNMENTS

RESULT 1
LOCUS A74271 1297 bp DNA linear PAT 15-OCT-1999
DEFINITION Sequence 1 from Patent W09401565.
ACCESSION A74271
VERSION A74271.1 GI:6064296
KEYWORDS
SOURCE
ORGANISM

Coriander.
Coriandrum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Coriandrum.
REFERENCE
1 (bases 1 to 1297)
MURPHY, D.J. and FAIRBAIRN, D.J.
GENES FOR ALTERING PLANT METABOLISM

Db 781 AAATCGTGGAGAGCTTCCGAGATTCAGCCAGACCACTGTTATCCGATTTTCTGAC 840
OY 901 ATGATGCGCAAAAAATATACATATGCCAGGCACTGATATAGCAGGAGTGCAGACT 960
Db 841 AAGATGAGGAAGAAATATAGCAATGCCAGCTCATGCAATGTAGGAGGCTCCGATGATG 900
OY 961 CTTTTTAAACATTTTACGCGGCTGCTCAGAGAGTGGGCTTATCTCCGTTGATTA 1020
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OY 1081 GAGCAGGGGCGAAAGCGAGGAATATGTTGATTTGGGTCGCCAAGATTAGCGAGT 1140
Db 1021 GGTGAAAGGAGAAAGGCTCAGAGATATGTTTGTAGCTTGGCTGTGATCAGAGAGAT 1080
OY 1141 CAAGAGAAAGTGCAGGGAGGAAGAGAAAGAAAGCTAGCAGCCCTGTTCTTTCAG 1200
Db 1081 GAGGAGAAAGTTCAGAGGCAAG-----AGAGAAAGCTGTGTGCTGTGGCTTTCAG 1134
OY 1201 TGGATTTTCAATCGGAGGATTTGAAGATATGA 1230
Db 1135 TGGATTTTCAACCGTCAGATCATCATATGA 1164

RESULT 4

RCCSACPD

LOCUS

DEFINITION Ricinus communis stearyl-acyl-carrier protein desaturase mRNA, 3'

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

POBMED

FEATURES

source

Location/Qualifiers

1..1643

/organism="Ricinus communis"

/db_xref="taxon:3988"

/tissue_type="seed"

/dev_stage="developing"

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BASE COUNT 462 a 321 c 383 g 477 t

ORIGIN

Query Match 42.7%; Score 573.8; DB 8; Length 1643;
Best Local Similarity 67.3%; Pred. No. 6.6e-129;
Matches 869; Conservative 0; Mismatches 393; Indels 30; Gaps 3;

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Db 1150	AGGAAGCTCGAAGACAGAGAGCTCAAGGAAGGCGCAAG-----GAAGCACCCACATG	1200		
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Db 1201	CTTTACACTGGATTTTTCGATAGGCAAGTGTGAGTGGCTAAAGTGCAGAGACGAA	1260		
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Db 1261	ACCGAAATGGTTAGTTTCATCTTTTCATGTC	1292		
RESULT 5				
LOCUS	RCSTEA	1662 bp	mRNA	linear
DEFINITION	R. communis stearyl-acyl carrier protein desaturase.			PLN 25-JUL-1991
ACCESSION	X56508			
VERSION	X56508.1	GI:21092		
KEYWORDS	carrier protein; stearyl-acyl.			
SOURCE	Ricinus communis.			
ORGANISM	Ricinus communis			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.			
AUTHORS	1 (bases 1 to 1662)			
TITLE	Knutzon, D.S.			
REFERENCE	Direct Submission			
AUTHORS	Submitted (08-NOV-1990) D.S. Knutzon, CALGENE INC, 1920 FIFTH STREET, DAVIS CA 95616, USA			
TITLE	2 (bases 1 to 1662)			
REFERENCE	Knutzon, D.S., Scherer, D.E. and Schreckengost, W.E.			
AUTHORS	Nucleotide sequence of a complementary DNA clone encoding stearyl-acyl carrier protein desaturase from castor bean, Ricinus Communis			
TITLE	1. 1662			
JOURNAL	Plant Physiol. 96, 344-345 (1991)			
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LOCUS 190191 1668 bp DNA linear PAT 10-AUG-1998

DEFINITION Sequence 15 from patent US 5723595.

ACCESSION 190191

VERSION 190191.1 GI:3410131

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1668)

AUTHORS Thompson, G.A. and Knaut, V.C.

TITLE Plant desaturases--compositions and uses

JOURNAL Patent: US 5723595-A 15 03-MAR-1998;

FEATURES

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BASE COUNT 464 a 325 c 386 g 493 t

ORIGIN

Query Match 42.6%; Score 572; DB 6; Length 1668;

Best Local Similarity 69.1%; Pred. 1.8e-128;

Matches 823; Conservative 0; Mismatches 341; Indels 27; Gaps 2;

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RESULT 7

SSMSACPD 1580 bp mRNA linear PLN 01-FEB-2000

LOCUS

DEFINITION Sesame mRNA for stearyl-acyl carrier protein desaturase, complete cds, clone CDS01.

ACCESSION D42086

VERSION D42086.1 GI:575941

KEYWORDS stearyl-acyl carrier protein desaturase.

SOURCE Sesamum indicum (strain:4294) seed, cell expansion stage cDNA to mRNA, clone lib:lambda gt10 clone:CDS01.

ORGANISM Sesamum indicum

REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.

AUTHORS Yukuwa, Y., Takaiwa, F., Shoji, K., Masuda, K. and Yamada, K.

TITLE 1 (bases 1 to 1580)

STRUCTURE and expression of two seed-specific cDNA clones encoding stearyl-acyl carrier protein desaturase from sesame, Sesamum indicum L.

JOURNAL Plant Cell Physiol. 37 (2), 201-205 (1996)

MEDLINE 96213006

REFERENCE 2 (bases 1 to 1580)

AUTHORS Yamada, K.

TITLE Direct Submission

JOURNAL Submitted (12-NOV-1994) Kyoto Yamada, Toyama University, Faculty of Science, Biology; Gofuku 3190, Toyama, Toyama 930, Japan (E-mail: yamada@sci.toyama-u.ac.jp, Tel: 0764-41-1271 (ex. 2335), Fax: 0764-41-2972)

FEATURES

source 1..1580

Location/Qualifiers


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Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
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REFERENCE
AUTHORS
Chopra, V.L.
TITLE
Transgenic expression of cDNA encoding steroyl acyl carrier protein
desaturase of sesamum indicum in indian mustard
JOURNAL
Unpublished
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AUTHORS
Chopra, V.L.
TITLE
Transgenic indian mustard high in oleate
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Direct Submission
JOURNAL
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New Delhi, 110012, INDIA
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Db 1325 GAGTAGAAGAGAAAGATGTG 1346

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LOCUS AF051134
DEFINITION Macfadyena unguis-cati acyl-ACP desaturase (fad1) mRNA, complete
cds
ACCESSION AF051134

VERSION AF051134.1 GI:2944443
KEYWORDS Macfadyena unguis-cati.
SOURCE Macfadyena unguis-cati.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Bignoniaceae; Macfadyena.
REFERENCE 1 (bases 1 to 1509)
AUTHORS Cahoon, E.B., Shah, S., Shanklin, J. and Browse, J.
TITLE A Determinant of Substrate Specificity Predicted from the Acyl-ACP Desaturase of Developing Doxantha Seed
JOURNAL Plant Physiol. (1998) In press
REFERENCE 2 (bases 1 to 1509)
AUTHORS Cahoon, E.B., Shah, S., Shanklin, J. and Browse, J.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1998) IBC, Washington State University, Pullman, WA 99164-6340, USA
FEATURES
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Oy 85 CTTGCTCGTTTCTTAAGTACCATTTACAGTGCAGAGTGTAGCTCCAAAGGTTTTC 144
Db 98 CCCAAATGCTCTTCTTTTGAAGCTTCCCGCAGTGTGCTCAGATCTTCAAGCTTTC 157
Oy 145 ATGGCTTCACTGTCAACTCTTAACCTCATGCTTCTTGATATATCTCAAA----- 193
Db 158 GTGGCTCCACTCTCTGCTTGTGAGGAGTGTGAGACCGCAGAGAAACTTTTATG 217
Oy 194 -----GTCCGCCCAATCTTCAAGTACATCTCATGCTTGTGATATATCTCAAA----- 246
Db 218 CTGACAGTAGGCTGCTGTTTCAAGTATACACACTTATGAGCAGACACCAAAATTTGATC 277
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DEFINITION	Thunbergia alata clone pTAl delta-9 stearyl-acyl carrier protein desaturase mRNA, partial cds.	007552.1	GI:533081	Thunbergia alata.	Thunbergia alata.
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AUTHORS	Cahoon, E.B., Becker, C.K., Shanklin, J. and Ohlrogge, J.B.				
TITLE	CDNA's for isoforms of the delta 9-stearyl-acyl carrier protein desaturase from Thunbergia alata endosperm				
JOURNAL	Plant Physiol. 106 (2), 807-808 (1994)				
MEDLINE	95083771				

FEATURES	source
REFERENCE	PUBMED
AUTHORS	2 (bases 1 to 1319)
TITLE	Cahoon, E. B.
JOURNAL	Direct Submission
	Submitted (08-MAR-1994) Cahoon E. B., Brookhaven National Laboratory, Biology, Upton, NY 11973, USA
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DEFINITION complete cds.
ACCESSION M83199
VERSION M83199.1 GI:169894
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Caryophyllales; Caryophyllales; Simmondsiaceae; Simmondsia.
REFERENCE 1 (bases 1 to 1576)
AUTHORS Sato, A., Becker, C.K. and Knauf, V.C.
TITLE Nucleotide sequence of a complementary DNA clone encoding
stearyl-acyl carrier protein desaturase from Simmondsia chinensis
JOURNAL Plant Physiol. 99, 362-363 (1992)
FEATURES
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 QY 466 TCTATGCTCAATAGGTGTGATGATTTAAGATGAGACTGGGGCTGAGCCCAAGTCTTG 525
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Comogen Ltd.

OM protein - protein search, using sw model

Run on: December 1, 2002, 21:18:46 ; Search time 35 Seconds

(without alignments)
2319.502 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: sp_fungi:*
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5: sp_invertebrate:*
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7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1424	69.1	396	10	Q93X20 sesamum ind
5	1401.5	68.0	401	10	Q39355 brassica na
6	1395	67.7	396	10	Q24497 helianthus
7	1391.5	67.5	401	8	Q9XOR7 brassica ju
8	1384.5	67.1	409	10	Q9SW87 arachis hyp
9	1381.5	67.0	401	10	Q22832 arabidopsis
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11	1377	66.8	396	10	Q9M4N5 gossypium h
12	1371	66.5	396	10	Q65040 mactadema
13	1370.5	66.5	396	10	Q8S059 oryza sativ
14	1365	66.2	358	10	Q43196 thunbergia
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23	1347.5	65.3	407	10	Q42591	Q42591 arabidopsis
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26	1262.5	61.2	386	10	Q947F2	Q947F2 kochia scop
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33	1171.5	56.8	385	10	P92933	P92933 asclepias s
34	1106	53.6	387	10	Q41510	Q41510 thunbergia
35	831	40.3	222	10	Q64906	Q64906 pelargonium
36	635	30.8	161	10	Q9XFH1	Q9XFH1 elaeis guin
37	609.5	29.6	167	10	Q43142	Q43142 sesamum ind
38	295	14.3	328	16	Q9XAL3	Q9XAL3 streptomyce
39	271.5	13.2	338	16	Q50050	Q50050 mycobacteri
40	256.5	12.4	338	16	Q8VXD4	Q8VXD4 mycobacteri
41	256.5	12.4	338	16	Q50824	Q50824 mycobacteri
42	153	7.4	170	2	Q9K539	Q9K539 mycobacteri
43	142.5	6.9	828	12	Q9WRP6	Q9WRP6 macaca mula
44	135	6.5	275	16	Q9X793	Q9X793 mycobacteri
45	122.5	5.9	2269	5	Q26223	Q26223 plasmodium

ALIGNMENTS

RESULT 1
Q43140 ID Q43140 PRELIMINARY; PRT; 396 AA.
AC Q43140;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase precursor (EC 1.14.99.6)
DE (Stearoyl-ACP desaturase).
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-4294;
RX MEDLINE=96213006; PubMed=8665096;
RA Yukawa Y., Takaiwa F., Shoji K., Masuda K., Yamada K.;
RT "Structure and expression of two seed-specific cDNA clones encoding
RT stearoyl-acyl carrier protein desaturase from sesame, Sesamum indicum
RT L.";
RL Plant Cell Physiol. 37:201-205(1996).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL, D42086; BAA07681.1; -.
DR HSSP, P22337; 1AFL.
DR InterPro; IPR005067; FA_desat.

DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF03405; FA_desaturase.2; 1.
 DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
 KW Transl. peptide.
 FT TRANSIT 34 33 POTENTIAL.
 FT CHAIN 1 396 STEAROYL-ACYL CARRIER PROTEIN DESATURASE.
 SO SEQUENCE 396 AA; 45168 MW; A23475AB676A0940 CRC64;

Query Match 70.7%; Score 1457; DB 10; Length 396;
 Best Local Similarity 69.5%; Pred. No. 4,2e-104;
 Matches 280; Conservative 50; Mismatches 57; Indels 16; Gaps 4;

OY 1 MALKL---NFQCKKNHPAFAKSPDPVTRVSSPRVMASTVNSNWLDLTKSPN---- 53
 DB 1 MALKLAINFQSKPCSPFLP---PVASVRSRPFMASTLRSGSKVEETVKRPNP 56

OY 54 --LQVTHSMPPQKLEIFKALSDMARNVLIHLKSVESKMPDYLDPVSDGFEQYREL 111
 DB 57 VHVQVTHSMPPQKLEIFKALSDMARNVLIHLKSVESKMPDYLDPVSDGFEQYREL 116

OY 112 RERAKETPDYFVVLVGDMTTEALPTYSMLNRCGDKETGAEPSAMAMTPTAAE 171
 DB 117 RERAKETPDYFVVLVGDMTTEALPTYSMLNRCGDKETGAEPSAMAMTPTAAE 176

OY 172 NRHGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGITYSFOERATFISH 231
 DB 177 NRHGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGITYSFOERATFISH 236

OY 232 ANTKLAQHYGDKNLAIHIGSISASDEKRNATYTKIVEKLAIDPDTTVAIFADMRKI 291
 DB 237 GNTARLARHEDDLKLAQICGTIADDEKRNATYTKIVEKLEIDPNDTVLAIFADMRKI 296

OY 292 TMPAHLMYDSDELFFKFTVAQRYVXSALDYCDLLEFLVDKNVRLGLSDEGRKA 351
 DB 297 SMPAHLMYDGRDNLFFHSSVAQRLGYTAKDADILEHLVARKVANTLGLSADGRKA 356

OY 352 QEYVCELGPKTRVREKYGKREKKKAHPVSFWIFNREKI 394
 DB 357 QDYVCELGPKTRVREKYGKREKKKAHPVSFWIFNREKI 396

RESULT 2
 ID 043141 PRELIMINARY; PRT: 396 AA.

AC 043141;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Sesamum indicum (Oriental sesame) (gingelly).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
 OX NCBI_TaxID=4182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4294;
 RA Yukawa Y., Takaiwa F., Yamada K.;
 RT "Structure and expression of two cDNA clones encoding stearyl-acyl carrier protein desaturase in sesame."
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: STEAROYL-(ACYL-CARRIER PROTEIN) + AH(2) + O(2) = OLEOYL-(ACYL-CARRIER PROTEIN) + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 DR EMBL: D49832; BA008635.1; -.
 DR HSP; P22337; IAFR.
 DR InterPro: IPR005067; FA_desat.
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF03405; FA_desaturase.2; 1.
 DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
 KW Transl. peptide.
 SO SEQUENCE 396 AA; 45212 MW; 1335DEC4A1B2BF9A CRC64;

Query Match 70.1%; Score 1446; DB 10; Length 396;
 Best Local Similarity 69.2%; Pred. No. 2,9e-103;
 Matches 279; Conservative 49; Mismatches 59; Indels 16; Gaps 4;

OY 1 MALKL---NFQCKKNHPAFAKSPDPVTRVSSPRVMASTVNSNWLDLTKSPN---- 53
 DB 1 MALKLAINFQSKPCSPFLP---PVASVRSRPFMASTLRSGSKVEETVKRPNP 56

OY 54 --LQVTHSMPPQKLEIFKALSDMARNVLIHLKSVESKMPDYLDPVSDGFEQYREL 111
 DB 57 VHVQVTHSMPPQKLEIFKALSDMARNVLIHLKSVESKMPDYLDPVSDGFEQYREL 116

OY 112 RERAKETPDYFVVLVGDMTTEALPTYSMLNRCGDKETGAEPSAMAMTPTAAE 171
 DB 117 RERAKETPDYFVVLVGDMTTEALPTYSMLNRCGDKETGAEPSAMAMTPTAAE 176

OY 172 NRHGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGITYSFOERATFISH 231
 DB 177 NRHGDLLNKLYLSGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGITYSFOERATFISH 236

OY 232 ANTKLAQHYGDKNLAIHIGSISASDEKRNATYTKIVEKLAIDPDTTVAIFADMRKI 291
 DB 237 GNTARLARHEDDLKLAQICGTIADDEKRNATYTKIVEKLEIDPNDTVLAIFADMRKI 296

OY 292 TMPAHLMYDSDELFFKFTVAQRYVXSALDYCDLLEFLVDKNVRLGLSDEGRKA 351
 DB 297 SMPAHLMYDGRDNLFFHSSVAQRLGYTAKDADILEHLVARKVANTLGLSADGRKA 356

OY 352 QEYVCELGPKTRVREKYGKREKKKAHPVSFWIFNREKI 394
 DB 357 QDYVCELGPKTRVREKYGKREKKKAHPVSFWIFNREKI 396

RESULT 3
 ID 09SEK6 PRELIMINARY; PRT: 396 AA.

AC 09SEK6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Persea americana (Avocado).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
 OX NCBI_TaxID=3435;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_FUERTE;
 RA Madl L., Prusky D.;
 RT "Sequence of a cDNA Clone Encoding an Avocado (Persea americana) (delta9)- Stearoyl-Acyl Carrier Protein Desaturase (Accession No. AF116861)." (PGR99-167).
 RL Plant Physiol. 121:1054-1054(1999).
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: STEAROYL-(ACYL-CARRIER PROTEIN) + AH(2) + O(2) = OLEOYL-(ACYL-CARRIER PROTEIN) + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY

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CC SIMILARITY).
CC -I- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: AF116861; AAF15308.1; -.
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase.2; 1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transl. peptide.
SQ SEQUENCE 396 AA; 45454 MW; 0F971ABDC07C2AD7 CRC64;

Query Match 69.9%; Score 1441; DB 10; Length 396;
Best Local Similarity 67.6%; Pred. No. 7,1e-103;
Matches 273; Conservative 55; Mismatches 53; Indels 24; Gaps 6;

QY 1 MALKLNFOCKKNNHFAFAKSPLPV-----TRVSSPRVFMASTVNSNVLNKLKSPN---SP 51
DB 1 MALKLS-----PYMFQSKLPFLASYPSPMLRSPRVFMASSTLRSTKEVDNKKPSP 53
QY 52 P---NLQVTHSNPPOKLEIFKSLDDMARNNVLHLKSVKSWQPODYLDPVSDGFEQY 108
DB 54 PREVHQVTHSNPPOKLEIFKSLDDMARNNVLHLKSVKSWQPODYLDPVSDGFEQY 113
QY 109 RELRRAREIPDDYFVVLGDMTEALPTYSMLNRCGIDEGAEPSANAMTRAT 168
DB 114 BELRRAREIPDDYFVVLGDMTEALPTYSMLNRCGIDEGAEPSANAMTRAT 173
QY 169 AENRHGDLNKLKYLKSLGVDNRKIEKTYOYLIGSGMDIKSENSPYLGFYTSFOERATF 228
DB 174 AENRHGDLNKLKYLKSLGVDNRKIEKTYOYLIGSGMDIKSENSPYLGFYTSFOERATF 233
QY 229 ISHAHTAKLAQHYGDKNLAHICGSIASDEKRAHTATYKIVEKLAETDPTTYAIFADMMRK 288
DB 234 ISHGHTARAKKYGDKLAKICGTIAADEKRHEATYKIVEKLEFIDPDYGVLAFCDDMK 293
QY 289 KITTPAHLMYDGSDELKFKHTAAVAQRYVYVSLDYCDLLEFLVKNMVERLTGLSDEG 348
DB 294 KITSPAHLMYDGDDELFGHFSSVAORLGVYAKDYADILELVARKNVHLLTGLSPSG 353
QY 349 RKAQYVCELGPKIRVEEKVOGKEKKKAEPH-VSFWSIFNRELKI 394
DB 354 KTAQEFICKLAPRIRSLERARSRAK---EGPTIPFSWIFNREVKL 396

RESULT 4
Q93X20 PRELIMINARY; PRT; 396 AA.
AC Q93X20:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Stroyl acyl carrier protein.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=DEVELOPING SEED;
RA Kanrar S.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=DEVELOPING SEED;
RA Chopra V.L.;
RL "Transgenic expression of cDNA encoding steroyl acyl carrier protein
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RT desaturase of sesamum indicum in Indian mustard.";
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=DEVELOPING SEED;
RA Chopra V.L.;
RL "Transgenic Indian mustard high in oleate.";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ313331; CAC44792.1; -.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase.2; 1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; UNKNOWN.1.
SQ SEQUENCE 396 AA; 45054 MW; 4945DFAC687BB2 CRC64;

Query Match 69.1%; Score 1424; DB 10; Length 396;
Best Local Similarity 67.7%; Pred. No. 1,5e-101;
Matches 273; Conservative 53; Mismatches 61; Indels 16; Gaps 4;

QY 1 MALKL--NFQCKNNHFAFAKSPLPVTRVSSPRVFMASTVNSNVLNKLKSPN---SP 53
DB 1 MALKLAINFQSPKCSFALP---PVASVSPKPFVASTLFGSKKEVETVKRPFPRE 56
QY 54 --LQVTHSNPPOKLEIFKSLDDMARNNVLHLKSVKSWQPODYLDPVSDGFEQYREL 111
DB 57 VHQVTHSNPPOKLEIFKSLDDMARNNVLHLKSVKSWQPODYLDPVSDGFEQYREL 116
QY 112 REKAREIPDDYFVVLGDMTEALPTYSMLNRCGIDEGAEPSANAMTRAT 171
DB 117 REKAREIPDDYFVVLGDMTEALPTYSMLNRCGIDEGAEPSANAMTRAT 176
QY 172 NRHGDLNKLKYLKSLGVDNRKIEKTYOYLIGSGMDIKSENSPYLGFYTSFOERATF 221
DB 177 NRHGDLNKLKYLKSLGVDNRKIEKTYOYLIGSGMDIKSENSPYLGFYTSFOERATF 236
QY 232 ANAKLAQHYGDKNLAHICGSIASDEKRAHTATYKIVEKLAETDPTTYAIFADMMRK 291
DB 237 GNTARLAREHGDKLAKICGTIAADEKRHEATYKIVEKLEFIDPDYGVLAFCDDMK 296
QY 292 TTPAHLMYDGSDELKFKHTAAVAQRYVYVSLDYCDLLEFLVKNMVERLTGLSDEGKA 351
DB 297 SMPAHLMYDGRDNLKDFHSSVAORLGVYAKDYADILELVARKNVHLLTGLSAGQKA 356
QY 352 QQYVCELGPKIRVEEKVOGKEKKKAEPH-VSFWSIFNRELKI 394
DB 357 QDVYVCELGPRIIRLEBRAQRAKAP---KIPPSWVHREVQL 396

RESULT 5
Q93935 PRELIMINARY; PRT; 401 AA.
AC Q93935:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP
DE desaturase).
GN BN4.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. JET NEUF;
RA MEDLINE=94286739; PubMed=8016261;
RA Slocumbe S.P., Piffanelli P., Fairbairn D., Bowra S., Hatzopoulos H.,
RA Tsiantis M., Murphy D.J.;
RL "Temporal and tissue specific regulation of a Brassica napus stearyl-
RT acyl carrier protein desaturase gene.";
RL Plant Physiol. 104:1167-1176(1994).
CC -I- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
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CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
 -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
 -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
 -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
 -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 EMBL: X74782; CAA52786.1; -.
 DR HSSP: P22337; IAFR.
 DR InterPro: IPR005067; FA_desat.
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF03405; FA_desaturase_2; 1.
 DR PROSITE: PS00574; FATTY ACID DESATUR_2; 1.
 DR Chloroplast: Fatty acid biosynthesis; NADP: Oxidoreductase;
 KW Transil peptide.
 SQ SEQUENCE 401 AA; 45482 MW; 1CCFB15626270401 CRC64;

Query Match 68.0%; Score 1401.5; DB 10; Length 401;
 Best Local Similarity 65.4%; Pred. No. 8e-100;
 Matches 265; Conservative 66; Mismatches 59; Indels 15; Gaps 5;

OY 1 MALKNFQCKNHHPADAKSPLYTRVSSPR-VMAST-----VNSNMVLDNLKSP----- 51
 1 MALKNLFASQPKLPSSARP-PISTLRSPKFLCLASSSSPALSSSTKEVESLKRPPTP 59
 DB 1 MALKNLFASQPKLPSSARP-PISTLRSPKFLCLASSSSPALSSSTKEVESLKRPPTP 59
 OY 52 --PILQVTHSWPQOKLEIFKSLDMDARRNNVLHLKSVKSNQPODYLPDPVSDGFEQVR 109
 60 KEVAVQVLSHPQOKLEIFKSLDMDARRNNVLHLKSVKSNQPODYLPDPVSDGFEQVR 119
 DB 60 KEVAVQVLSHPQOKLEIFKSLDMDARRNNVLHLKSVKSNQPODYLPDPVSDGFEQVR 119
 OY 110 ELERAKEIPDDYFVVLVGMITEALPTVMSLNRCGIDETGAEPSSAMAMTRAWTA 169
 120 ELRRARRELDDYFVVLVGMITEALPTVMTNLTLDGVRDETCASPTSAWVTRAWTA 179
 DB 120 ELRRARRELDDYFVVLVGMITEALPTVMTNLTLDGVRDETCASPTSAWVTRAWTA 179
 OY 170 EENRHGDLNKLKYLSCGVDMRKLEKTIQYLLIGSGMDIKSENSPYLGFYTSFORATFI 229
 180 EENRHGDLNKLKYLSCGVDMRKLEKTIQYLLIGSGMDIKSENSPYLGFYTSFORATFI 239
 DB 180 EENRHGDLNKLKYLSCGVDMRKLEKTIQYLLIGSGMDIKSENSPYLGFYTSFORATFI 239
 OY 230 SHANTAKLAQHYGDKNLAHIGSISASDEKRRHATATYKIVKLAIEDPPTVIAFADMRRK 289
 240 SHGNTARAKHSGDKLAQICGTIADDEKRRHATATYKIVKLEIDPDGTVAFAFADMRRK 299
 DB 240 SHGNTARAKHSGDKLAQICGTIADDEKRRHATATYKIVKLEIDPDGTVAFAFADMRRK 299
 OY 290 KITPRAHLMDGSDLELFKFTTAVAAQRYVXSALDYCDILEFLVDKMNVERLTGLSDGR 349
 300 KISMPAHLMDGSDLELFKFTTAVAAQRYVXSALDYCDILEFLVDKMNVERLTGLSDGR 359
 DB 300 KISMPAHLMDGSDLELFKFTTAVAAQRYVXSALDYCDILEFLVDKMNVERLTGLSDGR 359
 OY 350 KAOEYVCELGPRIKRVKEKVGKKEKKKAHPVSFSWIFENRETKI 394
 360 KAOEYVCELGPRIKRVKEKVGKKEKKKAHPVSFSWIFENRETKI 401
 DB 360 KAOEYVCELGPRIKRVKEKVGKKEKKKAHPVSFSWIFENRETKI 401

RESULT 6

024497 PRELIMINARY; PRT: 396 AA.

ID 024497
 AC 024497;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Helianthus annuus (Common sunflower).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
 OC Heliantheae; Helianthus.
 OC NCBI_TaxID=4232;
 OX (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN=MAMMOTH;

RA Hongtrakul V., Slabaugh M.B., Knapp S.J.;
 RT "Sunflower stearyl-ACP desaturase."
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
 CC CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
 CC COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
 -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
 -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 EMBL: U01339; AAB65144.1; -.
 DR HSSP: P22337; IAFR.
 DR InterPro: IPR005067; FA_desat.
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF03405; FA_desaturase_2; 1.
 DR PROSITE: PS00574; FATTY ACID DESATUR_2; 1.
 DR Chloroplast: Fatty acid biosynthesis; NADP: Oxidoreductase;
 KW Transil peptide.
 SQ SEQUENCE 396 AA; 45128 MW; BC79CA9631952E11 CRC64;

Query Match 67.7%; Score 1395; DB 10; Length 396;
 Best Local Similarity 66.9%; Pred. No. 2.5e-99;
 Matches 267; Conservative 52; Mismatches 56; Indels 24; Gaps 4;

OY 16 AFANSPILPVR-----VSSPRVMASTVNSNMVLDNLKSP-----PNIQV 56
 2 ALRMSPVTLQREIYPSYTFHOSKNLRSLFAMASTIGSTPKVETKRPFPREVHLQV 61
 DB 2 ALRMSPVTLQREIYPSYTFHOSKNLRSLFAMASTIGSTPKVETKRPFPREVHLQV 61
 OY 57 THSNPQOKLEIFKSLDMDARRNNVLHLKSVKSNQPODYLPDPVSDGFEQVRRELERAK 116
 62 THSNPQOKLEIFKSLDMDARRNNVLHLKSVKSNQPODYLPDPVSDGFEQVRRELERAK 121
 DB 62 THSNPQOKLEIFKSLDMDARRNNVLHLKSVKSNQPODYLPDPVSDGFEQVRRELERAK 121
 OY 117 EIPDDYFVVLVGMITEALPTVMSLNRCGIDETGAEPSSAMAMTRAWTAENRRGD 176
 122 EIPDDYFVVLVGMITEALPTVMTNLTLDGVRDETCASPTSAWVTRAWTAENRRGD 181
 DB 122 EIPDDYFVVLVGMITEALPTVMTNLTLDGVRDETCASPTSAWVTRAWTAENRRGD 181
 OY 177 LINKLYLSGRVDMRKLEKTIQYLLIGSGMDIKSENSPYLGFYTSFORATFISHANTAK 236
 182 LHQYLYLSGRVDMRKLEKTIQYLLIGSGMDIKSENSPYLGFYTSFORATFISHANTAK 241
 DB 182 LHQYLYLSGRVDMRKLEKTIQYLLIGSGMDIKSENSPYLGFYTSFORATFISHANTAK 241
 OY 227 LAOHYGDKNLHIGSISASDEKRRHATATYKIVKLAIEDPPTVIAFADMRRKKTTPAH 296
 242 HAKDYGDLKLAQICGTIADDEKRRHATATYKIVKLEIDPDGTVAFAFADMRRKKTTPAH 301
 DB 242 HAKDYGDLKLAQICGTIADDEKRRHATATYKIVKLEIDPDGTVAFAFADMRRKKTTPAH 301
 OY 297 LMWDGSDLELFKFTTAVAAQRYVXSALDYCDILEFLVDKMNVERLTGLSDGRKAOEYVC 356
 302 LMWDGSDLELFKFTTAVAAQRYVXSALDYCDILEFLVDKMNVERLTGLSDGRKAOEYVC 361
 DB 302 LMWDGSDLELFKFTTAVAAQRYVXSALDYCDILEFLVDKMNVERLTGLSDGRKAOEYVC 361
 OY 357 ELGPRIKRVKEKVGKKEKKKAHP-VSFSWIFENRETKI 394
 362 ELGPRIKRVKEKVGKKEKKKAHP-VSFSWIFENRETKI 396
 DB 362 ELGPRIKRVKEKVGKKEKKKAHP-VSFSWIFENRETKI 396

RESULT 7

09X0R7 PRELIMINARY; PRT: 401 AA.

ID 09X0R7
 AC 09X0R7;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Brassica juncea (Leaf mustard) (Indian mustard).
 OS Chloroplast.
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

CC eurousids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PUSA JAIRISAN;
RA Vageshababu H.S., Kirtl P.B., Chopra V.L.;
RT "Nucleotide sequence of the coding region of the plastidic delta-9-
stearoyl-acyl carrier protein desaturase of Brassica juncea.";
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
= OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: AF153420; AAD40245.1; -
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2; 1.
DR PROSITE: PS00574; FATTY ACID DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 401 AA; 45504 MW; 1726DA429DCF00EB CRC64;
Query Match 67.5%; Score 1391.5; DB 8; Length 401;
Best Local Similarity 64.9%; Pred. No. 4.7e-99;
Matches 266; Conservative 58; Mismatches 61; Indels 25; Gaps 5;
QY 1 MALKL-----NFQCKNHPAFAKSP--LPVTVSSPRVEMASTVNSMVLNLSKS 50
DB 1 MALKLNPASQPIYSPSSARPPISFRSPKFLCLASSSP-----ALSSSTKEVESLKK 54
QY 51 P-----PNIQVTHSMPPQKLEIFKSLDDMANNVLIHLKSVESKQPODYLPDPVSQDF 104
DB 55 PPTPKREVHVOGLSMPPQKLEIFKSMEDMAEQNLITHLKDEKSMQPODFLPDPSQDF 114
QY 105 EEOYRELREARAKELPDYFVVLVGDMLTEBALPTYMSMLNRCDGKIDFGAPSAAMWT 164
DB 115 EDQYKELERARRELDPDYFVVLVGDMLTEBALPTYQTMINTLDGVRDEFGASPTFAAVWT 174
QY 165 RAMTAENRRHGDLLNKLYLSGRVDMRKIEKTYOYLIGSGMDIKSENSPYLGIYTSFOE 224
DB 175 RAMTAENRRHGDLLNKLYLSGRVDMRKIEKTYOYLIGSGMDPTENNPNYLGFIYTSFOE 234
QY 225 RATEFSHANTAKLAQHYGDKNLAHICGSIASDEKRHATATYTKVLEIDDPDTVIARA 284
DB 235 RATEFSHANTAKLAQHYGDKNLAHICGSIADCKRHEATATYTKVLEIDDPDTVIARA 294
QY 285 DMRRKKTTPAHMLMYDSDELTFKHFTVAQRYVYSAALDYCDILEFLVDMKNVERLTGL 344
DB 295 DMRRKKTTPAHMLMYDSDELTFKHFTVAQRYVYSAALDYCDILEFLVDMKNVERLTGL 354
QY 345 SDEGRKAQOYVCELGPKIRRYVEEKVQGEKKKAHEPVSFSWIFNELKI 394
DB 355 SDEGRKAQOYVCELGPKIRRYVEEKVQGEKKKAHEPVSFSWIFNELKI 401
RESULT 8
Q9SM87 PRELIMINARY; PRT; 409 AA.
AC Q9SM87;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP

DE desaturase).
OS Arachis hypogaea (Peanut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurousids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae;
OC Arachis.
OX NCBI_TaxID=3818;
RN [1]
RP SEQUENCE FROM N.A.
RC Tate P.L., Koehert G., Abbott A.G.;
RT "The phylogenetic relationship of the cultivated peanut (Arachis
hypogaea L.) to its wild relative based upon comparisons of stearoyl-
ACP desaturase sequences.";
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
= OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: AF17728; AAD48495.1; -
DR HSSP: P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2; 1.
DR PROSITE: PS00574; FATTY ACID DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transit peptide.
SQ SEQUENCE 409 AA; 46810 MW; 7C80926BD8534A58 CRC64;
Query Match 67.1%; Score 1384.5; DB 10; Length 409;
Best Local Similarity 66.3%; Pred. No. 1.7e-98;
Matches 274; Conservative 51; Mismatches 65; Indels 23; Gaps 7;
QY 1 MALKLN-----FOCKNHPAFAKSP--LPVTVSSPRVEMASTVNSMVLNLSKSP 51
DB 1 MALKLNPNPSQKLEIFSSSSSSSSSSSSSFLPQMASLRSPRFMASTLRTGSKSEVENLKKP 60
QY 52 -----PNIQVTHSMPPQKLEIFKSLDDMANNVLIHLKSVESKQPODYLPDPVSQDF 105
DB 61 PPTPKREVHVOGLSMPPQKLEIFKSLGMAEENILTLKRVKCMQPODYLPDPVSQDF 120
QY 106 EEOYRELREARAKELPDYFVVLVGDMLTEBALPTYMSMLNRCDGKIDFGAPSAAMWT 165
DB 121 EEOYRELREARAKELPDYFVVLVGDMLTEBALPTYQTMINTLDGVRDEFGASLTSMAVWR 180
QY 166 AMTAENRRHGDLLNKLYLSGRVDMRKIEKTYOYLIGSGMDIKSENSPYLGIYTSFOE 225
DB 181 AMTAENRRHGDLLNKLYLSGRVDMRKIEKTYOYLIGSGMDPTENNPNYLGFIYTSFOE 240
QY 226 ATFTISGNTARLAKKGHGDKNLAHICGSIASDEKRHATATYTKVLEIDDPDTVIARA 285
DB 241 ATFTISGNTARLAKKGHGDKNLAHICGSIASDEKRHATATYTKVLEIDDPDTVIARA 300
QY 286 MMRRKKTTPAHMLMYDSDELTFKHFTVAQRYVYSAALDYCDILEFLVDMKNVERLTGLS 345
DB 301 MMRRKKTTPAHMLMYDSDELTFKHFTVAQRYVYSAALDYCDILEFLVDMKNVERLTGLS 360
QY 346 DSGRKAQOYVCELGPKIRRYVEEKVQGEKKKAHEPVSFSWIFNELKI 394
DB 361 DSGRKAQOYVCELGPKIRRYVEEKVQGEKKKAHEPVSFSWIFNELKI 409
RESULT 9
Q22832 PRELIMINARY; PRT; 401 AA.
ID Q22832

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AC 022832:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP
desaturase).
GN At2G43710 OR SS12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Konning C.M., Koo H., Motil K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21374454; PubMed=11481500;
RA Kachroo P., Shanklin J., Shah J., Whittle E.J., Klessig D.F.;
RA "A fatty acid desaturase modulates the activation of defense signaling
RT pathways in plants."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9448-9453(2001).
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: AC002333; AAB64033.1; -
DR EMBL: AF395441; AAK65232.1; -
DR HSSP: P22337; IARF.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2.1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2.1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW Transl peptidase.
SQ SEQUENCE 401 AA: 45693 MW; 0C46984578D4E1D1 CRC64;

Query Match 67.0%; Score 1381.5; DB 10; Length 401;
Best Local Similarity 65.7%; Pred. No. 2.8e-98;
Matches 266; Conservative 61; Mismatches 63; Indels 15; Gaps 6;

QY 1 MALKLNFOCKKNHPAFAKSPPLPVT-RVSSPR-VFMAST---VNSNSWVLDNLKSP----- 51
DB 1 MALKLN-PLVASQPKFPSPSTRPPIPSRPFELCLASSSPALSSGPKVESELKKRFTTP 59
QY 52 --PNIQVTHSMPPQKLETKSLDDMARNVLIHLKSVESKWPQDYLPPVSDGFEEDQYR 109
DB 60 REVHVOVLHSMPPQKLETKSMENNAEENLILHLKVERKSWQPODLPDPASGDFEDQYR 119
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QY 110 ELERAKELPDYEVVLVGDMTTEALPTYMSMLNRCOGIKDETGAEPSSAMAMTAWTA 169
DB 120 ELERARELPDDYFVVLVGDMTTEALPTYQTMINTLDGVRDETGAESPTSWAINTAWTA 179
QY 170 EENRHDDLNLKYLITISGRDMKRIEKTIOYLISGMDIKSENSPYLIGFTTSQERATFI 229
DB 180 EENRHDDLNLKYLITISGRDMRIEKTIOYLISGMDPRFENNPPYLGFITTSQERATFI 239
QY 230 SHNFTAKLQHYGDKMLNHTGSIASDEKRAHATYKRYKELAEIPDPTVIAFADMMRK 289
DB 240 SHONTARQAKHEHDIKLAQICGTIADDERKHEHATYKRYKELAEIPDPTVIAFADMMRK 299
QY 290 KITMPAHLWYDSDLLFKHFTAAQVRXYXSALDYCDLLEFLVDKWNERTLGLSDEGR 349
DB 300 KISMPAHLWYDSDNMLDFNFSVAQRLGYVYAKVDADILEFLVGRWKIDDLGLSGEGN 359
QY 350 KAOEYCEIGPKTRVEYKQEKKKKAEHPVSESMIFREKTI 394
DB 360 KAODYLGLAPRIKRIKIDERAQARAKKP--KIPFSWIDHREVOL 401

RESULT 10
Q94AE9 PRELIMINARY; PRT; 401 AA.
AC Q94AE9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE At2g43710/F18019.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Koesema E., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,
RA Banh J., Bowser L., Carlincl P., Dale J.M., Gibson H.A.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,
RA Kamliya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J.,
RA Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT Arabidopsis cDNA clones.
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carlincl P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamliya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY048233; AAK82496.1; -
DR EMBL: AY094014; AAM16170.1; -
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam: PF03405; FA_desaturase_2.1.
DR PROSITE: PS00574; FATTY_ACID_DESATUR_2.1.
SQ SEQUENCE 401 AA: 45692 MW; 01F09DD370F4E1D1 CRC64;

Query Match 67.0%; Score 1381.5; DB 10; Length 401;
Best Local Similarity 65.7%; Pred. No. 2.8e-98;
Matches 266; Conservative 61; Mismatches 63; Indels 15; Gaps 6;

QY 1 MALKLNFOCKKNHPAFAKSPPLPVT-RVSSPR-VFMAST---VNSNSWVLDNLKSP----- 51
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RESULT 11
024498
ID 024498 PRELIMINARY; PRT; 396 AA.

Query Match	67.0%;	Score 1381;	DB 10;	Length 396;
Best Local Similarity	66.5%;	Pred. No. 3e-98;		

RESULT 12	
Q9M4N5	
ID Q9M4N5	PRELIMINARY; PRT; 396 AA

DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;

KW Transit peptide.
 FT TRANSIT 1 32 POTENTIAL.
 CHAIN 33 396 AEE STEAROYL-ACP DESATURASE.
 SO SEQUENCE 396 AA; 45188 MW; 9F61C35A7363D9AB CRC64;

Query Match
 Best Local Similarity 66.8%; Score 1377; DB 10; Length 396;
 Matches 273; Conservative 40; Mismatches 76; Indels 12; Gaps 6;

1 MALKLNFQCKNHHP-AFAFASPLPVTYRVSPPVFMASVTNSNMYLDNLK---SPN--- 53
 1 MALNFNAIAKSKQKLPFCALPDKATLR--SPKFSMISTIPSGSKVEGVLKPKPTPEKVEP 58
 54 LQVTHSPMPQKLEIFKSLDDMARNNVLIHLKSVKSNQODYLPDPVSDGEEQVREL 113
 59 VQVTHSPMPKIEIFKSLLEGAEENNILLHLKPYEKQOPADFLDPDPSDGFHEQVREL 118
 114 RAKEIPDDYFVVLVGMITEALPTYSMLNRCDG;IKDETGAEPSSAMAMTWTAMTAEBN 173
 119 RAKEIPDDYFVVLVGMITEALPTYSMLNRCDG;IKDETGAEPSSAMAMTWTAMTAEBN 178
 174 HGLDLNKLYLISGRVDMRKTEKTIQVLLIGSGMDIKSENSPYLGFITYTSFOERATFISHN 233
 179 HGLDLNKLYLISGRVDMRKQIRTIQVLLIGSGMDPHTENSPYRGFIYTSFOERATFISHN 238
 234 TAKLAQHYGDKNLAHICGSIASDEKRNATATYKIVKLAELIDPDTYTAFAADMKKKTTM 293
 239 TGRLAKEVGDNLIAQICGSIASDEKRHEATATYKIVKLEFIDPDTYTAFAADMKKKTTM 298
 294 PAHLMYDGSDELFFKHFPAVAQRYVXSALDYCDLIEFLVDKMNVERLTGLSDGKRAQE 353
 299 PAEITPDYGRDNLFDHSSVAQRLGYTAKDYVDIEHLVGRMKKELAGLSAEGKRAQD 358
 354 YVCELGPRIKIRVEEKVGKSKKKAHEHVSFSWIFNRELKI 394
 359 YLCSLSPRIKIRLEERAQ--EKAKAP--SVPSWIDREVVL 396

RESULT 13
 ID 065040 PRELIMINARY; PRT; 396 AA.
 AC 065040;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Acyl-(acyl-carrier protein) desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 GN FAD1.
 OS Macfadyena unguis-cati.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Bignoniaceae; Macfadyena.
 OC NCBI_TaxID=73871;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cahoon E.B., Shah S., Shanklin J., Browse J.;
 RT "A Determinant of Substrate Specificity Predicted from the Acyl-ACP Desaturase of Developing Doxantha Seed.";
 RL Plant Physiol. 0:0-0(1998).
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: STEAROYL-(ACYL-CARRIER PROTEIN) + AH(2) + O(2) = OLEOYL-(ACYL-CARRIER PROTEIN) + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 * EMBL; AF051134; AAC05293.1; -.

DR HSSP; P22337; 1AER.
 DR InterPro; IPR005067; FA_desat.
 DR InterPro; IPR001225; FA_desaturase.
 DR Pfam; PF03403; FA_desaturase_2; 1.
 DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
 KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
 KW Transit peptide.
 SO SEQUENCE 396 AA; 45231 MW; 0101A758556D5C57 CRC64;

Query Match
 Best Local Similarity 66.5%; Score 1371; DB 10; Length 396;
 Matches 265; Conservative 60; Mismatches 62; Indels 16; Gaps 5;

1 MALKL---NFQCKNHHPAFAFASPLPVTYRVSPPVFMASVTNSNMYLDNLK---SPN--- 52
 1 MALKLNAINFEQ----SPKSSFGLEPVPVLSRPSKSVATILRSGLRDVEYFKTFSPARE 56
 53 -NLQVTHSPMPQKLEIFKSLDDMARNNVLIHLKSVKSNQODYLPDPVSDGEEQVREL 111
 57 VHVQVTHSMAPOKTEIFKAMEDMAENNILLHLKVEKCPQDQFLDPDASDFHQVREL 116
 112 RERAKEIPDDYFVVLVGMITEALPTYSMLNRCDG;IKDETGAEPSSAMAMTWTAMTAEB 171
 117 RERAKEIPDDYFVVLVGMITEALPTYSMLNRCDG;IKDETGAEPSSAMAMTWTAMTAEB 176
 172 NRHGLDLNKLYLISGRVDMRKTEKTIQVLLIGSGMDIKSENSPYLGFITYTSFOERATFISH 231
 177 NRHGLDLNKLYLISGRVDMRKQIRTIQVLLIGSGMDPHTENSPYLGFITYTSFOERATFISH 236
 232 ANTAKLAQHYGDKNLAHICGSIASDEKRNATATYKIVKLAELIDPDTYTAFAADMKKKTTM 291
 237 GNTARLARHGGDFKLAQICGSIASDEKRHEATATYKIVKLEFIDPDTYTAFAADMKKKTTM 296
 292 TPAHLMYDGSDELFFKHFPAVAQRYVXSALDYCDLIEFLVDKMNVERLTGLSDGKRA 351
 297 SNPDHFMIDGRDNLFDHSSVAQRLGYTAKDYVDIEHLVGRMKKELAGLSAEGKRA 356
 352 QEVCELGPRIKIRVEEKVGKSKKKAHEHVSFSWIFNRELKI 394
 357 QDVYCGLPRIKIRLEERAQIRAKQAPR--LPFSWIDREVVL 396

RESULT 14
 ID 08S059 PRELIMINARY; PRT; 396 AA.
 AC 08S059;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative stearoyl-acyl-carrier protein desaturase.
 GN P0678F11.19.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsunoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone: P0678F11.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003437; BAB86112.1; -.
 SO SEQUENCE 396 AA; 44875 MW; 2A3C588505FF6DD CRC64;

Query Match
 Best Local Similarity 66.5%; Score 1370.5; DB 10; Length 396;
 Matches 256; Conservative 53; Mismatches 51; Indels 9; Gaps 4;

31 RYFMASTVNSNMYLDNLK---SPN---NLQVTHSPMPQKLEIFKSLDDMARNNVLIHLK 85
 32 RYFMAVNS-GAVSTRKVENKKRFPARREVHVQVTHSPMPQKLEIFKSLDDMARNNVLIHLK 90

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 1, 2002, 21:18:11 ; Search time 14 Seconds

(without alignments)
1167.262 Million cell updates/sec

Title: US-09-732-597-2

Perfect score: 2062

Sequence: 1 MALKNFOCKKNHPAFKAS.....KKKAHPVFSWIFNRELKI 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1545.5	75.0	385	1	STAD_CORSA
2	1490	72.3	396	1	STAD_RICCO
3	1422.5	69.0	411	1	STAD_SOYBN
4	1412	68.5	396	1	STAD_CUCSA
5	1410.5	68.4	399	1	STAD_SPIOL
6	1406	68.2	396	1	STAD_CARTI
7	1396	67.7	398	1	STAD_BRANA
8	1386.5	67.2	393	1	STAD_SOLCO
9	1386.5	67.2	399	1	STAS_BRANA
10	1385.5	67.2	393	1	STAD_SOLTV
11	1385	67.2	390	1	STAD_OLEEU
12	1375.5	66.7	397	1	STAD_GOSHI
13	1373	66.6	393	1	STAD_ELACY
14	1360	66.0	398	1	STAD_STWCH
15	1352	65.6	396	1	STAD_HELNA
16	1310.5	63.6	390	1	STAD_ORYSA
17	1246	60.4	396	1	STAD_LINUS
18	114.5	5.6	1557	1	DVAL_DICVI
19	108	5.2	616	1	K329_METVA
20	105.5	5.1	393	1	TRPB_HELPY
21	102.5	5.0	393	1	Y044_UREPA
22	99	4.8	782	1	VATC_METMA
23	98	4.8	861	1	LOX3_PEA
24	97.5	4.7	607	1	HTRPG_FUSNN
25	96.5	4.7	607	1	PEPL_HUMAN
26	96.5	4.7	1756	1	TUL3_MOUSE
27	96	4.7	460	1	RA50_SULTO
28	96	4.7	879	1	NADA_BACSU
29	95	4.6	368	1	MYS3_SCHPO
30	95	4.6	2104	1	CCCL_DROME
31	94.5	4.6	524	1	YPY4_CAEEL
32	94.5	4.6	1163	1	SAP_HUMAN
33	93	4.5	524	1	P07602 h proactiva

34	92.5	4.5	574	1	ZDS_NARPS	049901 narcissus p
35	92.5	4.5	1255	1	DIAL_MOUSE	008808 mus musculu
36	92	4.5	526	1	VPS_BT11	P34476 bluetongue
37	92	4.5	886	1	RA50_ARCFU	029230 archaeoglob
38	91.5	4.4	426	1	TUB1_CAEEL	009306 caenorhabd1
39	91.5	4.4	1875	1	MLPI_YEAST	002455 saccharomyc
40	91.5	4.4	3685	1	DMD_HUMAN	P11532 homo sapien
41	91.5	4.4	3898	1	POIG_HCVA	P19712 hog cholera
42	91	4.4	552	1	NCAE_TPMV	095450 tupatia para
43	91	4.4	821	1	PPSA_PYRHO	057830 pyrococcus
44	91	4.4	1148	1	YK00_CAEEL	P34305 caenorhabd1
45	91	4.4	2472	1	SPCN_RAT	P16086 rattus norv

ALIGNMENTS

RESULT 1	STAD_CORSA	STANDARD	PRT	385 AA.
AC	P32063			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Omega-12 acyl-[acyl-carrier protein] desaturase, chloroplast precursor (EC 1.14.99.6).			
DE	Coriandrum sativum (Coriander).			
OC	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids II: Apiales: Apiaceae: Coriandrum.			
OX	NCBI_TaxID=4047;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Endosperm;			
RX	MEDLINE=93087491; PubMed=1454797;			
RA	Caahon E.B., Shanklin J., Ohlrogge J.B.;			
RT	"Expression of a coriander desaturase results in petroselinic acid production in transgenic tobacco."			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:11184-11188(1992).			
CC	-1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)			
CC	-1- Oleoyl-[acyl-carrier protein] + A + 2 H(2)O.			
CC	-1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.			
CC	-1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE			
CC	OILS. SPECIFICALLY INVOLVED IN THE SYNTHESIS OF PETROSELINIC ACID.			
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY)			
CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF			
CC	NONPHOTOSYNTHETIC TISSUES.			
CC	-1- TISSUE SPECIFICITY: FOUND ONLY IN TISSUES WHICH SYNTHESIZE			
CC	PETROSELINIC ACID, SUCH AS DEVELOPING SEEDS.			
CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.			
CC	-----			
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CC	EMBL: M93115; AAC63059.1; -			
DR	PIR: A47245; A47245.			
DR	HSSP: P22337; IAFR.			
DR	InterPro: IPR005067; FA_desat.			
DR	InterPro: IPR001225; FA_desaturase.			
DR	Pfam: PF03405; FA_desaturase_2; 1.			
KW	PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.			
KW	Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;			
KW	Transit peptide.			
FT	CHAIN 1 36 CHLOROPLAST (BY SIMILARITY).			
FT	TRANSIT 37 385 OMEGA-12 ACYL-[ACYL-CARRIER PROTEIN]			
FT	CHAIN 37 385 DESATURASE.			
SQ	SEQUENCE 385 AA; 43805 MM; AF759BFB6946EF03 CRC64;			

Query Match 75.0%: Score 1545.5; DB 1; Length 385;
 Best Local Similarity 73.1%: Pred. No. 3.8e-107;
 Matches 296; Conservative 42; Mismatches 36; Indels 31; Gaps 5;

1 MALKIN-----FOCKKNHPAFAKSPDPYRVSSP-----RVEMASTVNSNSMYLDLKK 49
 1 MAMLNALMTIQQCKRN-----MFTRIAPQAGRVRSKVSMASTLHASPLVFDKIK 51
 50 SPPLQVTHSPPOKLEIFKSLDDMARNNVLIHLKSVESKMPQDYLPPPTSDAFEDQYK 109
 52 AG-----RPEVDELFSLEGWARDNITLVHLSVENSQMPQDYLPPPTSDAFEDQYK 102
 110 FLERAKELPDYFVVLVGDMTTEALPTVMSLNKRCGDKDETGAEPSAMAMWTRAMTA 169
 103 EKREKAKIDPDEYFVVLVGDMTTEALPTVMSLNKRCGDKDETGAEPSAMAMWTRAMTA 162
 170 EENRHGDLNKKYLYLSGRVDMRKTEKTIQYLYLGSGMDIKSENSPYLGFITYTSFOERATFI 229
 163 EENRHGDLNKKYLYLSGRVDMRKTEKTIQYLYLGSGMDIKSENSPYLGFITYTSFOERATFI 222
 230 SHANTAKLAQHGDGKRLAHIGCSIASDEKRNATATYKIEKLAIDPDTTVAIFADMMRK 289
 223 SHANTAKLAQHGDGKRLAHIGCSIASDEKRNATATYKIEKLAIDPDTTVAIFADMMRK 282
 290 KITPMHMLYDGSDELLFHFHTAVAGRVXYVSALDYCDILEFLVDKMNVRRLGLSDEGR 349
 283 KIOMPAHMYDGSDDMLFHFHTAVAGRVXYVSALDYCDILEFLVDKMNVRRLGLSDEGR 342
 350 KAOEYVCELGPKTRVREKVOGKKKKAHPYFSFWMFNRKLI 394
 343 KAOEYVCSIAKTRVEKVOGKE--KKAFLVAFSFIIFNRKLI 385

RESULT 2
 STDAD_RICCO STANDARD; PRT; 396 AA.
 ID STDAD_RICCO P22357;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ACYL-[acyl-carrier protein] desaturase, chloroplast precursor
 (EC 1.14.99.6) (Stearoyl-ACP desaturase) (Delta(9) stearoyl-acyl
 carrier protein desaturase).
 OS Ricinus communis (castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
 NCBI_TaxID=3988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91172837; Pubmed=2006187;
 RA Shanklin J., Somerville C.R.;
 RT "stearyl-acyl-carrier-protein desaturase from higher plants is
 structurally unrelated to the animal and fungal homologs.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Endosperm;
 RA Knutzen D.S., Scherer D.E., Schreckengost W.E.;
 RT "Nucleotide sequence of a complementary DNA clone encoding stearyl-
 acyl carrier protein desaturase from castor bean, Ricinus communis.";
 RL Plant Physiol. 96:344-345(1991).
 RN [3]
 RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RA MEDLINE=97015109; Pubmed=8861937;
 RA Lindqvist Y., Huang W., Schneider G., Shanklin J.;
 RT "Crystal structure of delta9 stearoyl-acyl carrier protein desaturase
 from castor seed and its relationship to other di-iron proteins.";
 RL EMBO J. 15:4081-4092(1996).
 CC -I- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CHAIN.

CC -I- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
 CC -I- OLEOYL-[acyl-carrier protein] + A + 2 H(2)O.
 CC -I- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC -I- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
 CC OILS.
 CC -I- SUBUNIT: HOMODIMER.
 CC -I- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
 CC NONPHOTOSYNTHETIC TISSUES.
 CC -I- TISSUE SPECIFICITY: HIGHER LEVELS IN DEVELOPING SEEDS THAN IN LEAF
 CC AND ROOT TISSUES.
 CC -I- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC
 DR EMBL: M59857; AAA74692.1; ALT_INIT.
 DR EMBL: X56508; CAA39859.1; .
 DR PIR: S16463; OHCSAD.
 DR PIR: A39170; A39170.
 DR PDB: 1AER; 15-MAY-97.
 DR InterPro: IPR005067; FA_desat.
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF03405; FA_desaturase.2; 1.
 DR PROSITE: PS00574; FATTY ACID DESATURASE 2; 1.
 DR Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
 KW Transnit peptide; 3D-structure.
 FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 34 396 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
 SQ SEQUENCE 396 AA; 45371 MW; E50d472596392AF CRC64;

Query Match 72.3%: Score 1490; DB 1; Length 396;
 Best Local Similarity 71.1%: Pred. No. 5e-103;
 Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;

1 MALKIN-FOCKKNHPAFAKSPDPYRVSSP-----RVEMASTVNSNSMYLDLKKP-----PN 53
 1 MALKINPPLSQTKRLPSPALPMASTR--SPKFYMASTLKSGSKVENLKKPMPREYH 58
 54 LQVTHSPPOKLEIFKSLDDMARNNVLIHLKSVESKMPQDYLPPPTSDAFEDQYK 113
 59 VQVTHSPPOKLEIFKSLDDMARNNVLIHLKSVESKMPQDYLPPPTSDAFEDQYK 118
 114 RAKEIPDDYFVVLVGDMTTEALPTVMSLNKRCGDKDETGAEPSAMAMWTRAMTAENR 173
 119 RAKEIPDDYFVVLVGDMTTEALPTVMSLNKRCGDKDETGAEPSAMAMWTRAMTAENR 178
 174 HGDLNKKYLYLSGRVDMRKTEKTIQYLYLGSGMDIKSENSPYLGFITYTSFOERATFI 233
 179 HGDLNKKYLYLSGRVDMRKTEKTIQYLYLGSGMDIKSENSPYLGFITYTSFOERATFI 238
 234 TAKLAQHGDGKRLAHIGCSIASDEKRNATATYKIEKLAIDPDTTVAIFADMMRKKTIM 293
 239 TAKLAQHGDGKRLAHIGCSIASDEKRNATATYKIEKLAIDPDTTVAIFADMMRKKTIM 298
 294 PAHLMYDGSDELLFHFHTAVAGRVXYVSALDYCDILEFLVDKMNVRRLGLSDEGRKAOE 353
 299 PAHLMYDGSDDMLFHFHTAVAGRVXYVSALDYCDILEFLVDKMNVRRLGLSDEGRKAOE 358
 354 YVCELGPKTRVREKVOGKKKKAHP-VSFSWMFNRKLI 394
 359 YVCELGPKTRVREKVOGKKKKAHP-VSFSWMFNRKLI 396

RESULT 3
 STDAD_SOTBN STANDARD; PRT; 411 AA.
 ID STDAD_SOTBN Q42807;
 CC

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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
GN ACIDP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen L., Moon Y., Shanklin J., Nikolau B.J., Atherly A.G.:
RT "Cloning and sequence of a cDNA encoding stearyl-acyl carrier
RT protein desaturase from glycine max.";
RL (In) Plant Gene Register PGR95-105.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L34346; AAA92462.1; -.
CC DR HSSP; P22337; IAFR.
CC DR InterPro: IPR005067; FA_desat.
CC DR InterPro: IPR001225; FA_desaturase.
CC Pfam; PF03405; FA_desaturase_2; 1.
CC DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
CC Transf. peptide.
CC KW TRANSIT.
CC FT CHAIN.
CC FT 29 411 CHLOROPLAST (BY SIMILARITY).
CC FT SEQUENCE 411 AA; 47282 MW; 2727C3EDC8C97BA8 CRC64;
CC -----
Query Match 69.0%; Score 1422.5; DB 1; Length 411;
Best Local Similarity 67.7%; Pred. No.5.2e-98;
Matches 274; Conservative 46; Mismatches 54; Indels 31; Gaps 4;
QY 1 MALKINFOCKKNHPAAFKSPLPVTRVS-----SPRFVMASTVNSNSVNLNLKSP- 51
Db 1 MALRLN-----PIPTQTSFQPMASLRSPFRMASTVSSKKEVNIMKRF 46
QY 52 -----PNIQVYTHSMPPQKLETFKSLDDMARNNVLIHLKSVKSWQPDYLDPPVSDGFE 106
Db 47 TPPEEVHVOVYTHSMPPQKLETFKSLDDMARNNVLIHLKSVKSWQPDYLDPPVSDGFE 106
QY 107 QVRELREKRAKELPDYFVVLGDMTTEELALPYVMSMLRCDSIKRETKAEPSAMAMTR 166
Db 107 QVRELREKRAKELPDYFVVLGDMTTEELALPYVMSMLRCDSIKRETKAEPSAMAMTR 166
QY 167 WTAENRRHGDLNLKLYLSGRVDMKRIEKTIOYLLGSGMDIKSENSPYLGFIYTSFOERA 226
Db 167 WTAENRRHGDLNLKLYLSGRVDMKRIEKTIOYLLGSGMDIKSENSPYLGFIYTSFOERA 226
QY 227 TFIISANTAKLAQYIGDKNLAHIGCSIASDEKRAATVATYKVIKLAIEDPDTVTIAFAD 285
Db 227 TFIISANTAKLAQYIGDKNLAHIGCSIASDEKRAATVATYKVIKLAIEDPDTVTIAFAD 285

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Db	227	TFISIGNTARLAKHEGDIKIAQICGMISDKEHRTATATKIVEKLFESDPDGTWAFADM	286
Qy	287	MRRKITTPEAHLMYDGSDELLFKHFTAVAAQRYVYSALDYCILFEYLDKMNVERLTGLSD	346
Db	287	MRRKTTAMPAHMLYDGRDNLFDNNYSVAQIRIGVYAKYADYALIEFLYGRMKVEOLTGLSG	346
Qy	347	EGRKAQEVVCELGRIRRVEEKVQCKEKKKAENHVSYSWJFNRE	391
Db	347	EGRKAQEVYICGLPPIRIRLEERAQARVESST--LKFSWIDRE	388
RESULT 4			
STAD.	CUCSA	STANDARD:	PRT: 396 AA.
ID	STAD_CUCSA		
AC	P32061;		
DT	01-OCT-1993 (Rel. 27, Last sequence update)		
DT	01-OCT-1993 (Rel. 27, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Acyl-[acyl-carrier protein] desaturase, chloroplast precursor		
DE	(EC 1.14.99.6) (Stearoyl-ACP desaturase).		
OS	Cucumis sativus (Cucumber).		
CC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
CC	eurosidia I; Cucurbitales; Cucurbitaceae; Cucumis.		
OX	NCBI_TaxID=3659;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Seedling cotyledon;		
RA	Shanklin J., Mullins C., Somerville C.R.;		
RT	"Sequence of a complementary DNA from Cucumis sativus L. encoding the		
RT	stearoyl-acyl-carrier protein desaturase.";		
RL	Plant Physiol. 97:467-468(1991).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=91172837; PubMed=2006187;		
RA	Shanklin J., Somerville C.;		
RT	"Stearoyl-acyl-carrier-protein desaturase from higher plants is		
RT	structurally unrelated to the animal and fungal homologs.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).		
CC	-1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A		
CC	CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL		
CC	CHAIN.		
CC	-1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)		
CC	= Oleoyl-[acyl-carrier protein] + A + 2 H(2)O.		
CC	-1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.		
CC	-1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY		
CC	ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE		
CC	OILS.		
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF		
CC	NONPHOTOSYNTHETIC TISSUES.		
CC	-1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY		
CC	-----		
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CC	-----		
CC	EMBL: M59858; AAA33130.1; -.		
DR	PIR: B39170; B39170.		
DR	HSSP: P22337; IAFR.		
DR	InterPro: IPR005067; FA_desat.		
DR	InterPro: IPR001225; FA_desaturase.		
DR	Pfam: PF03405; FA_desaturase_2; 1.		
DR	PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.		
KW	Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;		
KW	Transit peptide.		
FT	TRANSIT	1	33
FT	CHAIN	34	396
FT	CONFLICT	114	114
FT			CHLOROPLAST (BY SIMILARITY).
FT			ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
FT			R -> V (IN REF. 2).

```

FT CONFLICT 290 290 E -> D (IN REF. 2)
SQ SEQUENCE 396 AA; 45583 MW; 2E19E894C106D4C8 CRC64;
Query Match 68.5%; Score 1412; DB 1; Length 396;
Best Local Similarity 66.6%; Pred. No. 2.9e-97;
Matches 271; Conservative 51; Mismatches 61; Indels 24; Gaps 5;

OY 1 MALKLNFOCKKNHPAFAKSPLEPVTR-----VSSPRVFMASVNSNSMYLNLKSP---51
DB 1 MALKE-----HPLTQSQPKLPSPFMPOLASLRSPKFWASTLRSRSEVETLKKRFMP 53
OY 52 ----PNIQVTHSMPPQKLEIFKSLDDMARNVLIHLKSVKSNOPDYLPPVSDGFEEOY 108
DB 54 PREVHQVTHSMPPQKMEIFKSLDDMARNVLIHLKSVKSNOPDYLPPVSDGFEEOY 113
OY 109 RELREKAKEIPDDYFVVLVGMITEALPTYSMLNRCIDKDETGAPESAMAMTRAWT 168
DB 114 RELREKAKEIPDDYFVVLVGMITEALPTYSMLNRCIDKDETGAPESAMAMTRAWT 173
OY 169 AEENRHGDLNKKYLYLSGRVDMRKIEKTIQYLIIGSGMDIKSENSPYIGFIYTSFOERATF 228
DB 174 AEENRHGDLNKKYLYLSGRVDMRKIEKTIQYLIIGSGMDIKSENSPYIGFIYTSFOERATF 233
OY 229 ISHANTATLAOHGDKNLAIHIGSISASDEKRNATYATKYVEKLAIEDPDPTVIAFADMMR 288
DB 234 ISHANTATLAOHGDKNLAIHIGSISASDEKRNATYATKYVEKLAIEDPDPTVIAFADMMR 293
OY 289 KRTMPAHMLMYGSDDELFFKHTFAVAORVYXSALDYCDILEFLVDMKNVERLTGLSDEG 348
DB 294 KRTMPAHMLMYGSDDELFFKHTFAVAORVYXSALDYCDILEFLVDMKNVERLTGLSDEG 353
OY 349 RKAQEVYCELGPKIRRVEEKVQGEKKKKAHEP-VSFSWTFNREIKI 394
DB 354 RKAQEVYCELGPKIRRVEEKVQGEKKKKAHEP-VSFSWTFNREIKI 396

RESULT 5
STAD_SPTOL
ID STAD_SPTOL STANDARD; PRT; 399 AA.
AC P28645;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Biroflea; TISSUE=Colyledon;
RX MEDLINE=92329733; PubMed=1627785;
RA Beppu T., Nishida I., Matsuo T., Murata N.;
RT *Nucleotide sequence of a cDNA clone encoding a precursor to
stearyl-[acyl-carrier-protein] desaturase from spinach, Spinacia
oleracea.
RL Plant Mol. Biol. 19:711-713(1992).
CC -1- FUNCTION: CONVERTS STEARYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + A(2) + O(2)
= oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
OILS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
NONPHOTOSYNTHETIC TISSUES.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.

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CC -----
DR EMBL; X62898; CAAA4687.1; -
DR PIR; S22480; OHSPAD.
DR HSSP; P22337; IAFR.
DR InterPro; IPR005067; FA_desat.
DR InterPro; IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase-2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KW Transf. peptide.
FT TRANSIT 1
FT CHAIN 36
FT SEQUENCE 399 AA; 45663 MW; 59B5E0609EA7CCC CRC64;

Query Match 68.4%; Score 1410.5; DB 1; Length 399;
Best Local Similarity 67.2%; Pred. No. 3.8e-97;
Matches 273; Conservative 59; Mismatches 55; Indels 19; Gaps 8;

OY 1 MALKLN-----FOCKKNHPAFAKSPLEPVTRVSSPRVFMASVNSNS-MVLDNLK---SP 51
DB 1 MALNLNPNVSTPFQCR--LPFSFSPROTSPRR--SPKFFMASTLSSSSPKAESESLKKPSP 56
OY 52 P---NLIQVTHSMPPQKLEIFKSLDDMARNVLIHLKSVKSNOPDYLPPVSDGFEEOY 108
DB 57 PREVHQVTHSMPPQKMEIFKSLDDMARNVLIHLKSVKSNOPDYLPPVSDGFEEOY 116
OY 109 RELREKAKEIPDDYFVVLVGMITEALPTYSMLNRCIDKDETGAPESAMAMTRAWT 168
DB 117 RELREKAKEIPDDYFVVLVGMITEALPTYSMLNRCIDKDETGAPESAMAMTRAWT 176
OY 169 AEENRHGDLNKKYLYLSGRVDMRKIEKTIQYLIIGSGMDIKSENSPYIGFIYTSFOERATF 228
DB 177 AEENRHGDLNKKYLYLSGRVDMRKIEKTIQYLIIGSGMDIKSENSPYIGFIYTSFOERATF 236
OY 229 ISHANTATLAOHGDKNLAIHIGSISASDEKRNATYATKYVEKLAIEDPDPTVIAFADMMR 288
DB 237 VSHGNSARLAKEHGLKMAQIGIITASDEKRNATYATKYVEKLAIEDPDPTVIAFADMMR 296
OY 289 KRTMPAHMLMYGSDDELFFKHTFAVAORVYXSALDYCDILEFLVDMKNVERLTGLSDEG 348
DB 297 KRTMPAHMLMYGSDDELFFKHTFAVAORVYXSALDYCDILEFLVDMKNVERLTGLSDEG 356
OY 349 RKAQEVYCELGPKIRRVEEKVQGEKKKKAHEP-VSFSWTFNREIKI 394
DB 357 RKAQEVYCELGPKIRRVEEKVQGEKKKKAHEP-VSFSWTFNREIKI 399

RESULT 6
STAD_CARTI
ID STAD_CARTI STANDARD; PRT; 396 AA.
AC P22243;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
OS Carthamus tinctorius (Safflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids II; Asterales; Asteraceae; Cardueae; Carthamus.
OX NCBI_TaxID=4222;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=91172850; PubMed=2006194;
RA Thompson G.A., Scherer D.E., Foxall-Van Aken S., Kenny J.W.,

```

RA Young H.L., Shintani D.K., Kridel J.C., Knauf V.C.;
 RT "Primary structures of the precursor and mature forms of
 RT stearoyl-acyl carrier protein desaturase from safflower embryos and
 RT requirement of ferredoxin for enzyme activity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2578-2582(1991).
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CC CHAIN.
 CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
 CC = Oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
 CC OILS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
 CC NONPHOTOSYNTHETIC TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC -----
 CC EMBL: M61109; AAA3021.1; -
 CC PIR: A39173; A39173.
 CC DR HSSP: P22337; IAFR.
 CC DR InterPro: IPR005067; FA_desat.
 CC DR InterPro: IPR001225; FA_desaturase.
 CC Pfam: PF03405; FA_desaturase_2; 1.
 CC DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
 CC KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
 CC Transf. peptide.
 CC TRANSIT 1 33 CHLOROPLAST
 CC FT CHAIN 34 396 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
 CC FT MOD_RES 34 34 BLOCKED (PARTIAL).
 CC SQ SEQUENCE 396 AA; 45054 MW; 7B14529889D39087 CRC64;

Query Match 68.2%; Score 1406; DB 1; Length 396;
 Best Local Similarity 67.1%; Pred. No. 8.2e-97;
 Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;

OY 1 MALKT--NFQCKKNHPAFAKSPLEPTRVSSPRVFMASTVNSMVLNLKSP----- 51
 DB 1 MALRTPTVTLQSEKRSFSEFFKK---ANLRSPKFMASLTGSTRKVDNAKPPPPRE 56
 OY 52 PVLQYTHSNPQKLEIFKSLDWMARNVLIHLKSVKSNQPODYLPDPVSDGFEQVREL 111
 DB 57 VHVQYTHSNPQKLEIFKSLDWMARNVLIHLKSVKSNQPODYLPDPVSDGFEQVREL 116
 OY 112 RRRAKEIPDDYVNVVIGMDITEALPTVMSMLNRGCIIDENGAESNAAMVRAATAEE 171
 DB 117 RRRAKEIPDDYVNVVIGMDITEALPTVMSMLNRGCIIDENGAESNAAMVRAATAEE 175
 OY 172 NRHGDLNKLTVLSGRVDMRKIEKTIQVYLGSGMDIKSENSPYLIGTYISFOERAFISH 231
 DB 177 NRHGDLNKLTVLSGRVDMRKIEKTIQVYLGSGMDIKSENSPYLIGTYISFOERAFISH 236
 OY 232 ANTKALAOHYGCKNLAHICGSIASDEKRNATYTKIVEKLAETIDPTVYIAEADMRRKKI 291
 DB 237 GNTAHAKHGKGVNLAQICGTIASDEKRHEATYTKIVEKLFEDIDPGTYLAFAADMRRKKI 296
 OY 292 TMPARILMDGSDLEFKHTTAAVQRYVXSALDYCDILEFVLDKMNVEVLGTGSDGKRA 351
 DB 297 SMPARILMDGSDLEFKHTTAAVQRYVXSALDYCDILEFVLDKMNVEVLGTGSDGKRA 356
 OY 352 QEVYCELGPRIKRVKEKVGKREKKAHP--VSFSWIFNRELKI 394
 DB 357 QGVYCGLPRIKRVKEKVGKREKKAHP--VSFSWIFNRELKI 396

RESULT 7
 STAD_BRA NA STANDARD; PRT; 398 AA.
 ID STAD_BRA NA STANDARD; PRT; 398 AA.
 AC P29108;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
 DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, R500;
 RX MEDLINE=92212861; PubMed=1557366;
 RA Knutson D.S., Thompson G.A., Radke S.E., Johnson W.B., Knauf V.C.,
 RA Kridel J.C.;
 RT "Modification of Brassica seed oil by antisense expression of a
 RT stearoyl-acyl carrier protein desaturase gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2624-2628(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, Jet neuf; TISSUE=leaf;
 RX MEDLINE=97260965; PubMed=9107041;
 RA Piffanelli P., Ross J.H., Murphy D.J.;
 RT "Intra- and extracellular lipid composition and associated gene
 RT expression patterns during pollen development in Brassica napus.";
 RL Plant J. 11:549-562(1997).
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CC CHAIN.
 CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
 CC = Oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
 CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
 CC OILS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
 CC NONPHOTOSYNTHETIC TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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 CC -----
 CC EMBL: X60978; CAA43294.1; -
 CC DR EMBL: X97325; CAA65990.1; -
 CC DR PIR: S23351; S23351.
 CC DR HSSP: P22337; IAFR.
 CC DR InterPro: IPR005067; FA_desat.
 CC DR InterPro: IPR001225; FA_desaturase.
 CC Pfam: PF03405; FA_desaturase_2; 1.
 CC DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
 CC KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
 CC Transf. peptide.
 CC TRANSIT 1 34 CHLOROPLAST (BY SIMILARITY).
 CC FT CHAIN 35 398 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
 CC SQ SEQUENCE 398 AA; 45347 MW; 9D0689FCFE41C5F5 CRC64;

Query Match 67.7%; Score 1396; DB 1; Length 398;
 Best Local Similarity 66.9%; Pred. No. 4.5e-96;
 Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;

OY 1 MALKLNQCK--NHPAFAKSPLEPTRVSSPRVFMASTVNSMVLNLKSP-----P 52

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Db      1 MALKLNPLASQPNFBSS -ARPTISFRSKFLCLCLASSSPALSSKRVESIKKPTTPREKV 59
QY      53 NLYQVTHSMPOCKITEIFESLDDMARNNVLTHLKSVEKSPQODYLPDPVSDGFEQVRELR 112
Db      60 HVOYLHSMPPQCKITEIFESMEDMAEONLLPQKDYKESWQPODELPPASDGDGEDQVRELR 119
QY      113 ERAKEIPDDYFVVLVGDMTTEALPYTMSLNLNCDGICKQETGAPESAMMMPTWPAEEN 172
Db      120 ERARELPDDYFVVLVGDMTTEALPYQYMLNLNDGVRDGTGSPISMAIWTWPAEEN 179
QY      173 RHGGLLNKKYLYLSGRVDMRKIEKTIQYLLISGMDIKSESPNYGFTYTSFOERATEFISHA 232
Db      180 RHGGLLNKKYLYLSGRVDMRKIEKTIQYLLISGMDPRENNPYLGLFTYTSFOERATEFISHG 239
QY      233 NTAKLAQHYGDKNLNHLICGSIASDEKRNATATYKYVKLAETDPDTYLAFAAMMRKIT 292
Db      240 NTAQAKHGHGLKLAQICGLTADDEKRNHETATYKYVKLEETDPDGTVMFAFAMMRKIS 299
QY      293 MPAHLMYQSGELLFKHETAVARQVXYASALDYCDLIEFLVDWNNYERLGLSDEGRKAQ 352
Db      300 MPAHLMYQSGRESLFDFNFSVAQGLYTTAKDYADLIEFLVGRKKLESLGLSGEGNKAQ 359
QY      353 EYVCELGPKIRRVEEKYQGGKRRKKAHEHPVSFIENRELKI 394
Db      360 EYLCGLTPRIRLDERAQAQAKGP--KVPFSWIHDRREVOL 398

RESULT 8
STAD_SOLCO          STANDARD;          PRT;          393 AA.
ID      SOLCO
AC      Q41319;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
        (EC 1.14.99.6) (Stearoyl-ACP desaturase).
DE      Solanum commersonii (Commerston's wild potato).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX      NCBI_TaxID=4109;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=leaf;
RA      Tribuci M., Grillo S., Costa A., Leone A.;
        Submitted (Apr-1994) to the EMBL/Genbank/DBJ databases.
CC      -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
        CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
        CHAIN.
CC      -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
        = Oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC      -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC      -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
        ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
        OILS.
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
        NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL, X78935; CA55535.1; -
DR      HSSP; P22337; IAFR.
DR      InterPro; IPR005067; FA_desat.
DR      InterPro; IPR001225; FA_desaturase.

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DR	PFAM: P03405: FA_desaturase_2:	NEG.
DR	PROSITE, PS00574: FATTY_ACID_DESATUR_2:	FALSE
KW	Oxidoreductase, Fatty acid biosynthesis, NADP: Chloroplast;	
FT	Transit peptide.	
FT	Transit 1	
FT	CHAIN 31 393	CHLOROPLAST (BY SIMILARITY)
FT	SEQUENCE 393 AA: 44765 MW: 5516E4E6B2C9501 CRC64;	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
Query Match	Best Local Similarity	Score 1386.5; DB 1: Length 393;
Matches 267; Conservative	66.3%; Pred. No. 2.2e-95;	53; Mismatches 64; Indels 19; Gaps
QY	1 MALKNTN---FQCKKHHNPAFAKSPLEVTYRVSSPRFMASTVNSNMVLDNLK---SP-	52
DB	1 MALNENSPFTQSIKT-----TRRCPSPLRSPRFMASTLRPSPVEDGNNKRPSPPRE	53
QY	53 -NLQVTHSPPOKLELFKSLDWMARNVYLHKSVKSMQPDQYLPDPYSDGFEQVREL	111
DB	54 VHVQVTHSPKPERKLEFSDLSHMADNNILGHKLPVKCKQASDELPRDASEGEQVREL	113
QY	112 RERAKETIPDQYFVLVAGDMLTEALPTYSMLNRCDGIDKDETGAESAMAMTRAWTAEE	171
DB	114 RERCKETIPDQYFVLVAGDMLTEALPTYSMLNRCDGIDKDETGAESAMAMTRAWTAEE	173
QY	172 NRHGLINKLYLISGRVDMRKLEKTYQLILGSGMDKSNSTYLGITYSPQERATFISH	231
DB	174 NRHGLINKLYLISGRVDMRKLEKTYQLILGSGMDPRTNNPLGLITYSPQERATFISH	233
QY	232 ANRATKLAOHGDNLNLIHIGSIASDEKRRHATATYTKIVERKLAIEDPTVYIAFADMMRKKI	291
DB	234 GNRARHAKHEGDKKLAVCGCIILADEKRHTATYTKIVERKLEFVDPDGTVALVADMMRKKI	293
QY	292 TMEPHLMTYDSDDELFKHTFAVARQRYXYVSALDYCIDLEFLVKKMNYERTLTGSDGKRA	351
DB	294 SMPHNLMTYDSDRDLNFHSTFAQRLGVYAKYVAIDLEFLVGRWELTKLTGSGGKRA	353
QY	352 QEYVCELGPKIRRYEERKQKRAEHVSFSWIFNELKI	394
DB	354 RDYVCGLAPRIKLEERQAARAKQA---PVPSWVGKRIKL	393
RESULT 9		
STAS_BRANA		
ID	STAS_BRANA	STANDARD: PRT: 399 AA.
AC	001771;	
DT	01-APR-1993 (Rel. 25, Created)	
DT	01-APR-1993 (Rel. 25, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Acyl-[acyl-carrier protein] desaturase, seed specific, chloroplast	
DE	precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase).	
OS	Brassica napus (Rape).	
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OS	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC	eurosid II; Brassicales; Brassicaceae; Brassica.	
OC	NCBI_TaxID=3708;	
OX	NCBI_TaxID=3708;	
RN	111	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=cv Jet neuf; TISSUE=Embryo;	
RX	MEDLINE=92385757; PubMed=1515603;	
RA	"Nicotiana S.P., Cummins I., Jarvis R.P., Murphy D.J.;	
RA	"Nucleotide sequence and temporal regulation of a seed-specific	
RT	Brassica napus cDNA encoding a stearoyl-acyl carrier protein (ACP)	
RT	desaturase.";	
RL	Plant Mol. Biol. 20:151-155(1992).	
CC	-i- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A	
CC	CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL	
CC	CHAIN.	
CC	-i- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)	
CC	= oleoyl-[acyl-carrier protein] + A + 2 H(2)O.	
CC	-i- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.	
CC	-i- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY	
CC	ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE	
CC	OILS.	


```
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Chloroplast (Probable).
CC -1- TISSUE SPECIFICITY: DEVELOPING SEED.
CC -1- DEVELOPMENTAL STAGE: INDUCED BY 25 DAYS AFTER ANTHESIS (DAA),
CC PEAKING AT 45 DAA BUT DECREASING CONSIDERABLY THEREAFTER.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X63364; CA444964.1; -.
DR PIR; S24995; S24995.
DR HSSP; P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KM Transit peptide.
FT TRANSIT 1 34 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 35 399 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
FT SEQUENCE 399 AA; 45358 MW; 8537254C13D9AF80 CRC64;
SQ
Query Match 67.2%; Score 1386.5; DB 1; Length 399;
Best Local Similarity 65.8%; Pred. No. 2.3e-95;
Matches 265; Conservative 59; Mismatches 66; Indels 13; Gaps 4;
QY 1 MALKLNFOCKKHPAFAFASPLPYTRVSSPRVFMASTVNS--NSMVLNLIKSP----- 51
DB 1 MALKFNPLVSGPYKLASSARP-PVSTFRSPFLCLASSSSPALSKVEESLKKPTPRE 59
QY 52 PNLQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVKSMQPODYLDPVSDGFEQVREL 111
DB 60 VHLQVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVKSMQPODYLDPVSDGFEQVREL 119
QY 112 RERAKEIPDDVFNVLVGMITEEALPTYSMLNRCDGIKDENGAEPSAMMTTAAEE 171
DB 120 RERARELPDDVFNVLVGMITEEALPTYSMLNRCDGIKDENGAEPSAMMTTAAEE 179
QY 172 NRHGDLLNKLYLSGRVDMRKTEKTIQYLIIGSGMDIKSENSPYLGFIYTSFQERATFISH 231
DB 180 NRHGDLLNKLYLSGRVDMRKTEKTIQYLIIGSGMDIKSENSPYLGFIYTSFQERATFISH 239
QY 232 ANTKAKLAOHYDGNLAHTCGSIASDEKRRHATYTKIVEKLAIEDPTTVIAFADMRKKI 291
DB 240 GNTARQAKHEHDLKLAQICGTIADEKRRHATYTKIVEKLEIDPDGTVAFAADMRRKI 299
QY 292 TMPAHLWYDGSDELLEFKHFTVAORVXYVSALDCCDILEFLVDKNNVRRLTGSDEGRKA 351
DB 300 SMPAHLWYDGSDELLEFKHFTVAORVXYVSALDCCDILEFLVDKNNVRRLTGSDEGRKA 359
QY 352 QEYVCELGPKIRRVEEKVQGEKKRKAHPYFSWIFNRELKI 394
DB 360 QEYVCELGPKIRRVEEKVQGEKKRKAHPYFSWIFNRELKI 399
RESULT 10
STAD_SOLITU STANDARD: PRT; 393 AA.
AC P46253;
DT 01-NOV-1995 (Rel. 32, Last Created)
DT 15-NOV-1995 (Rel. 32, Last sequence update)
DT 01-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (RC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_Taxid=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Taylor M.A., Smith S.B., Davies H.V., Burch L.R.;
RL Submitted (XXY-1992) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M91238; AAA33839.1; -.
DR HSSP; P22337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR001225; FA_desaturase.
DR Pfam; PF03405; FA_desaturase_2; 1.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
KM Transit peptide.
FT TRANSIT 1 30 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 31 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
FT SEQUENCE 393 AA; 44538 MW; 3FBCC28D57CA7FF CRC64;
SQ
Query Match 67.2%; Score 1385.5; DB 1; Length 393;
Best Local Similarity 64.5%; Pred. No. 2.7e-95;
Matches 258; Conservative 62; Mismatches 67; Indels 13; Gaps 4;
QY 1 MALKLNFOCKKHPAFAFASPLPYTRVSSPRVFMASTVNSMVLNLIKSP--SP--NL 54
DB 1 MALNTNGVSLKSHKML-----PPCCSSARSERPVMASTIRPSEVGSYKKAFTPREVHY 56
QY 55 QVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVKSMQPODYLDPVSDGFEQVRELRLER 114
DB 57 QVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVKSMQPODYLDPVSDGFEQVRELRLER 116
QY 115 AKIEIPDDVFNVLVGMITEEALPTYSMLNRCDGIKDENGAEPSAMMTTAAEENH 174
DB 117 AKIEIPDDVFNVLVGMITEEALPTYSMLNRCDGIKDENGAEPSAMMTTAAEENH 176
QY 176 GDLNKNLYLSGRVDMRKTEKTIQYLIIGSGMDIKSENSPYLGFIYTSFQERATFISHANT 234
DB 177 GDLNKNLYLSGRVDMRKTEKTIQYLIIGSGMDIKSENSPYLGFIYTSFQERATFISHANT 236
QY 235 AKLAOHYDGNLAHTCGSIASDEKRRHATYTKIVEKLAIEDPTTVIAFADMRKKITMP 294
DB 237 AKLAHEGDMKLAQICGTIADEKRRHATYTKIVEKLEIDPDGTVAFAADMRRKINSMP 296
QY 295 AHLWYDGSDELLEFKHFTVAORVXYVSALDCCDILEFLVDKNNVRRLTGSDEGRKAQCY 354
DB 297 AHLWYDGSDELLEFKHFTVAORVXYVSALDCCDILEFLVDKNNVRRLTGSDEGRKAQCY 356
QY 355 VCELGPKIRRVEEKVQGEKKRKAHPYFSWIFNRELKI 394
DB 357 VCELGPKIRRVEEKVQGEKKRKAHPYFSWIFNRELKI 393
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RESULT 11

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STAD_OLEU          STANDARD:          PRT:          390 AA.
ID STAD_OLEU
AC 045593;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
   (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Olea europaea (Common olive).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Oleaceae; Olea.
OX NCBI_TaxID=4146;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Leccino; TISSUE=Mesocarp;
RA Baldoni L., Georgi L., Abbott A.G.;
RT "Nucleotide sequence of a cDNA clone from Olea europaea encoding a
   stearyl-acyl carrier protein desaturase.";
RL (1) Plant Gene Register PGR96-052.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
   CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
   CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
   = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
   ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
   OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
   NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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   or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U58141; AAB67840.1; -.
CC HSSP: P22337; IAFR.
CC InterPro: IPR005067; FA.desat.
CC InterPro: IPR001225; FA.desaturase.
CC Pfam: PF03405; FA.desaturase.2; 1.
CC PROSITE: PS00574; FATTY ACID DESATUR_2; 1.
CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
   KM
   Transl. peptide.
   FT CHAIN 28 390 CHLOROPLAST (BY SIMILARITY). DESATURASE.
   FT TRANSIT 1 27 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
   SQ SEQUENCE 390 AA; 44596 MW; 39090EA32B7AC2E3 CRC64;

Query Match 67.2%; Score 1385; DB 1; Length 390;
Best Local Similarity 66.3%; Pred. No. 2.9e-95;
Matches 266; Conservative 55; Mismatches 62; Indels 18; Gaps 5;

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RESULT 12

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STAD_GOSHI          STANDARD:          PRT:          397 AA.
ID STAD_GOSHI
AC 042770;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
   (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. DeltaLine 16;
RA Liu Q., Singh S., Sharp P., Green A., Marshall D.R.;
RT "Nucleotide sequence of a cDNA from Gossypium hirsutum encoding a
   stearyl-acyl carrier protein desaturase.";
RL (1) Plant Gene Register PGR96-018.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
   CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
   CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
   = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
   ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
   OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
   NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
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CC -----
CC EMBL: X95988; CAA65232.1; -.
CC HSSP: P22337; IAFR.
CC InterPro: IPR005067; FA.desat.
CC InterPro: IPR001225; FA.desaturase.
CC Pfam: PF03405; FA.desaturase.2; 1.
CC PROSITE: PS00574; FATTY ACID DESATUR_2; 1.
CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
   KM
   Transl. peptide.
   FT CHAIN 34 397 CHLOROPLAST (BY SIMILARITY).
   FT TRANSIT 1 33 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
   SQ SEQUENCE 397 AA; 45233 MW; 5FAA220238B2C37A CRC64;

Query Match 66.7%; Score 1375.5; DB 1; Length 397;
Best Local Similarity 67.7%; Pred. No. 1.5e-94;

```

Matches 272: Conservative 41: Mismatches 76: Indels 13: Gaps 6:

QY 1 MALNLFQCKNHP-AAPAKSPLPYRVSSPRFVASTVNSMWLDNLK---SPN--- 53
 DB 1 MALNFAIASKSKLPKLPALPKATLR--SPKFSMSTRIPSCSEVGNLKKPFTPEKVP 58
 QY 54 LQVHSMRPOKLEIFKSLDDMARNNVLHLKSVKSMOPDYLPPVSGFEQVRELRE 113
 DB 59 VOITHSMRPHKIEFKSLGMAENNLHLKRVKRCQPADFLPPNSGCFHEQVRELRE 118
 QY 114 RAKEIPDDYFVVLVQDMITTEALPTYSMLNRCGIDKDEGAPESAMAMWTAMTAEEER 173
 DB 119 RAKEIPDDYFVVLVQDMITTEALPTYSMLNRCGIDKDEGAPESAMAMWTAMTAEEER 178
 QY 174 HGDLINKLYLSGRVDMRKIEKTIQYLLGSGMDIKSENSPYLGFITYTSQERATFISHAN 233
 DB 179 HGDLINKLYLSGRVDMRKIEKTIQYLLGSGMDIKSENSPYLGFITYTSQERATFISHAN 238
 QY 234 TAKLAQHYGDMKLAHICGSIASDEKRNATATYKIEKLAIDPDTVIAFADMMKKITM 293
 DB 239 TGRLAKEGVDINLAQICGSIASDEKRNATATYKIEKLAIDPDTVIAFADMMKKITAM 298
 QY 294 PAHMYADSDDELLFKHFTVAQRVYVSALDYCDILEFLVDKMWERTLGLSDEGRKAOE 353
 DB 299 PAEFTYDGRDINLDPHYSVAQRIYVYAKDYVDIVELVDMKKELAGLSAEGRKAOE 358
 QY 354 YVCELGPKIRVEEKVGKERRKKAHPVS-FSWIFNRELKI 394
 DB 359 YLCSLPISRIRLEERAQ---EKAQGSTVPSPSWIFDEVKL 397

RESULT 13
 STAD_ELAVY STANDARD: PRT: 393 AA.

AC 024428:
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
 DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS *Elaeis guineensis* var. *tenera* (oil palm).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: Liliopsida: Arecaeae: Arecoidae;
 OC Coccoae: Elaeidinae: Elaeis.
 OC NCBI_TaxID=51953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mesocarp:
 RA Shah F.H., Rashid O.;
 RT "Nucleotide sequence of a cDNA clone encoding stearoyl-acyl-carrier-
 protein from *Elaeis guineensis* var. *tenera*.";
 RL (In) Plant Gene Register PGR96-110.
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CHAIN.
 CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
 ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
 OILS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
 CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC EMBL: U68756; AAB41041.1; ALT_INIT.
 DR HSSP: P22337; IAFR.
 DR InterPro: IPR005067; FA_desat.
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF03405; FA_desaturase_2; 1.
 DR PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; NADP: Chloroplast;
 KW Transmembrane protein; Transmembrane protein; Transmembrane protein;
 KW TRANSIT 1 31 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 32 393 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
 SQ SEQUENCE 393 AA; 44857 MW; C6A8788B80D8A0CC CRC64;

Query Match 66.6%; Score 1373; DB 1; Length 393;
 Best local similarity 68.0%; Pred. No. 2.2e-94;
 Matches 264; Conservative 55; Mismatches 59; Indels 10; Gaps 6;

QY 14 PAAF-AKSPLEPYR-VSSPRFVASTVNSMWLDNLK---SPN---NLQYTHSMRPOKLE 66
 DB 9 PEAFLECFSPKRTTRSPRISMASTVSGPSTKVEIPKRPMPREYHVOYTHSMRPOKIE 68
 QY 67 IFKSLDMMARNNVLHLKSVKSMOPDYLPPVSDGFEQVRELREAKEIPDDYFVVL 126
 DB 69 IFKSLDMMARNNVLHLKSVKSMOPDYLPPVSDGFEQVRELREAKEIPDDYFVVL 128
 QY 127 VGDMITTEALPTYSMLNRCGIDKDEGAPESAMAMWTAMTAEEERHGDLLKLYL 186
 DB 129 VGDMITTEALPTYSMLNRCGIDKDEGAPESAMAMWTAMTAEEERHGDLLKLYL 188
 QY 187 RVDMMKIEKTIQYLLGSGMDIKSENSPYLGFITYTSQERATFISHANTAKLAHYGKNL 246
 DB 189 RVDMMKIEKTIQYLLGSGMDIKSENSPYLGFITYTSQERATFISHANTAKLAHYGKNL 248
 QY 247 AHICGSIASDEKRNATATYKIEKLAIDPDTVIAFADMMKKITPAHMYADSDDEL 306
 DB 249 AHICGSIASDEKRNATATYKIEKLAIDPDTVIAFADMMKKITPAHMYADSDDEL 308
 QY 307 FKHFTVAQRVYVSALDYCDILEFLVDKMWERTLGLSDEGRKAOEYCELGPKIRVE 366
 DB 309 FKHFTVAQRVYVSALDYCDILEFLVDKMWERTLGLSDEGRKAOEYCELGPKIRVE 368
 QY 367 EKVQGEKKKKAHPVSFSWIFNRELKI 394
 DB 369 ERAQ---ERAKQAPR-IPCSWITGREGVL 393

RESULT 14
 STAD_SIMCH STANDARD: PRT: 398 AA.

AC 001753:
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
 DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS *Simmondsia chinensis* (Jojoba).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
 OC Caryophyllales: Caryophyllales: Simmondsiaceae; Simmondsia.
 OC NCBI_TaxID=3999;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sato A., Becker C.K., Knaf V.C.;
 RT "Nucleotide sequence of a complementary DNA clone encoding stearoyl-
 acyl carrier protein desaturase from *Simmondsia chinensis*.";
 RL Plant Physiol. 99:362-363(1992).
 CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
 CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
 CHAIN.
 CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
 CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY

CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES.
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M83199; AAA3932.1; -
CC HSSP: P22337; IAFR.
CC InterPro: IPR005067; FA_desat.
CC Pfam: PF03405; FA_desaturase.2; 1.
CC PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
CC Transit peptide.
CC TRANSIT 1 34 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 35 398 ACTL-[ACTL-CARRIER PROTEIN] DESATURASE.
CC SEQUENCE 398 AA; 45130 MW; F3E000B04427D8 CRC64;
SQ
Query Match 66.0%; Score 1360; DB 1; Length 398;
Best Local Similarity 65.7%; Pred. No. 2, 1e-93;
Matches 266; Conservative 52; Mismatches 69; Indels 18; Gaps 6;
QY 1 MALKLNFOCKKNHPAFAKSPLEPVYTVSSPRVYMA-STVNSNSMVDNLKSP-----P 52
DB 1 MALKLN-HTFNFSMAVTSSGLPSRHYLRSHRVFMASSITGITSKELPNAPKPHMPPREA 59
QY NLOVTHSMPPQKLEIFKSLDMARNVLIHLKSVKSNQPODYLDPVSDGFEEQVREL 112
DB 60 HVQTHSMPPQKLEIFKSLDMARNVLIHLKSVKSNQPODYLDPVSDGFEEQVREL 119
QY 113 ERAKEIPDDYFVVLVGMITEEALPTVMSLNRCGDIKDTGABESAMAMTTRATAEN 172
DB 120 ERKEIPEDEVVLVGMITEEALPTVQTMNLTDGVNDEFGASLTISWAIATRAVTAEN 179
QY 173 RHGDLINKYLYLSGRVDMRKTEKTYOYLIGSGMDIKSENSPYLGFITYSPDERATFISHA 232
DB 180 RHGDLINKYLYLSGRVDMRKTEKTYOYLIGSGMDIKSENSPYLGFITYSPDERATFISHG 239
QY 233 NFAKLAOHYGCKNLAHIGSIADEKRRHATYTKIVEKLAIEDPTTYIAFADMMRRKKT 292
DB 240 NFAKLAOHYGCKNLAHIGSIADEKRRHATYTKIVEKLAIEDPTTYIAFADMMRRKKT 299
QY 293 MPAHLMTDGSDELLFKHFTAAVQRYVXSALDYCDILEFLVDKNNVRELTLGSDGKRAQ 352
DB 300 MPAHLMTDGSDELLFKHFTAAVQRYVXSALDYCDILEFLVDKNNVRELTLGSDGKRAQ 359
QY 353 EYVCELGPKIRREVEKVGKREKKRAEHPVS---FSWIFNRELKT 394
DB 360 EYVCELGPKIRREVEKVGKREKKRAEHPVS---FSWIFNRELKT 398

RESULT 15
STAD_HELAN STANDARD: PRT: 396 AA.

AC Q96436;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;

OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SWE3;
RA Coughlan S.J., Hastings C.E., Winfrey R.J.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN.
CC -1- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)
CC = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
CC -1- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
CC -1- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF
CC NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U70374; AAB09571.1; -
CC HSSP: P22337; IAFR.
CC InterPro: IPR005067; FA_desat.
CC Pfam: PF03405; FA_desaturase.2; 1.
CC PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
CC Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
CC Transit peptide.
CC TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 34 396 ACTL-[ACTL-CARRIER PROTEIN] DESATURASE.
CC SEQUENCE 396 AA; 45078 MW; 97E455A116791B81 CRC64;
SQ
Query Match 65.6%; Score 1352; DB 1; Length 396;
Best Local Similarity 66.0%; Pred. No. 8, 1e-93;
Matches 266; Conservative 51; Mismatches 70; Indels 16; Gaps 5;
QY 1 MALKLN---FOCKKNHPAFAKSPLEPVTVSSPRVYMASTVNSNSMVDNLKSP----- 51
DB 1 MAIRINTATFGSDLYRSFAPQ-PKP---LRSPKFMASITGATTKVSTKPKPTPPRE 56
QY 52 PNLQVTHSMPPQKLEIFKSLDMARNVLIHLKSVKSNQPODYLDPVSDGFEEQVREL 111
DB 57 VHQOVLHSMPPQKLEIFKSMGMAENNIIVHLKPEVKCQWADPLDPVSDGFEEQVREL 116
QY 112 KRAKEIPDDYFVVLVGMITEEALPTVMSLNRCGDIKDTGABESAMAMTTRATAEN 171
DB 117 KRAKEIPDDYFVVLVGMITEEALPTVQTMNLTDGVNDEFGATLTISWAIATRAVTAEN 176
QY 172 NRGDLINKYLYLSGRVDMRKTEKTYOYLIGSGMDIKSENSPYLGFITYSPDERATFISH 231
DB 177 NRGDLINKYLYLSGRVDMRKTEKTYOYLIGSGMDIKSENSPYLGFITYSPDERATFISH 236
QY 232 ANTKLAOHYGCKNLAHIGSIADEKRRHATYTKIVEKLAIEDPTTYIAFADMMRRKKT 291
DB 237 GNTARHAKHGHGVKLAOMCGIIAADKRRHETATYTKIVEKLAIEDPTTYIAFADMMRRKKT 296
QY 292 TWPBHLMTDGSDELLFKHFTAAVQRYVXSALDYCDILEFLVDKNNVRELTLGSDGKRA 351
DB 297 SMPBHLMTDGSDELLFKHFTAAVQRYVXSALDYCDILEFLVDKNNVRELTLGSDGKRA 356
QY 352 OEYVCELGPKIRREVEKVGKREKKRAEHPVSFSWIFNRELKT 394
DB 357 OEYVCELGPKIRREVEKVGKREKKRAEHPVSFSWIFNRELKT 396

Search completed: December 1, 2002, 21:20:34
Job time : 16 secs

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DR WPI: 1995-253884/33.
DR N-PSDB: AAQ92889.
XX New omega-12 desaturase from coriander - and DNA encoding it, useful
PT for making transgenic plants able to synthesise petroselinic acid.
XX
XX
PS Claim 4; Columns 18; 25pp; English.
XX A cDNA library prep. from developing seeds of coriander was
CC screened with a probe based on a partial cDNA clone (AAQ92888) of
CC omega-12 desaturase to isolate full-length clone EC201 (AAQ92889).
CC Expression of this cDNA in transgenic tobacco callus resulted in
CC prodn. of petroselinic acid (18:1 omega 12) and omega-12
CC hexadecenoic acid.
XX
XX Sequence 385 AA:
SQ
Query Match 75.0%; Score 1545.5; DB 16; Length 385;
Best Local Similarity 73.1%; Pred. No. 7.3e-140;
Matches 296; Conservative 42; Mismatches 36; Indels 31; Gaps 5;
OY 1 MALKLN-----FOCKKNHPAFAKSPLEPTRVSSP-----RVFMASTVNSNSVLDNLK 49
DB 1 MAMKLNALMTLQCPKRN-----MFRIRAPQAGRVASKVSMASTLHASPFLVFDK 51
OY 50 SPPNLOVTHSMPPQKLEIFKSLDDMARNNVLIHLKSVKSWQPODYLPDVSDFGEQVR 109
DB 52 AG-----RPEVDELFSLEGWARDNLTIVHLKSVENSWQPODYLPDPTSPAEEQVK 102
OY 110 ELREAKEIPDDYFVVLVGMITEEALPTYMSMLNRCQDKDETGAEPSSAMWTRAMTA 169
DB 103 EMERKADIPDEFVVLVGMITEEALPTYMSMLNRCQDKDETGAEPSSAMWTRAMTA 162
OY 170 EENRHGDLNKLKYLISGRVDMRKIEKTIOYLIGSGMDIKSENSPYLGFIYTSFOERATFI 229
DB 163 EENRHGDLNKLKYLISGRVDMRKIEKTIOYLIGSGMDIKSENSPYLGFIYTSFOERATFI 222
OY 230 SHANTAKLAOHYGDKNIAHIGSIASDEKRHAATYKIVEKLAIEDPTTVIAFADMMRK 289
DB 223 SHANTAKLAOHYGDKNIAHIGSIASDEKRHAATYKIVEKLAIEDPTTVIAFADMMRK 282
OY 290 KIMPPIHMYDGSDELFEKHFETAQORVXYYSALDYCDILEFLVDKNVVERLTGLSDEGR 349
DB 283 KIDMPHAMWDGSDMDLKFHFTAAQOIGVYSAMDYCDILEFLVDKNVVERLTGLSDEGR 342
OY 350 KAOEYVCELGPKIRVEEKVQGEKKKKAHPSPFSWTFNRRLKI 394
DB 343 KAOEYVCELGPKIRVEEKVQGEKKKKAHPSPFSWTFNRRLKI 385
RESULT 2
AAW44350 standard; Protein: 396 AA.
ID AAW44350
XX
XX AAW44350:
XX
XX 28-MAY-1998 (first entry)
XX
XX Ricinus communis desaturase from clone pCGN3230.
DE
XX Ricinus communis; castor bean; delta-9 desaturase; oilseed;
KM fatty acid saturation.
XX
XX Ricinus communis.
OS
XX US5723595-A.
XX
XX 03-MAR-1998.
XX
XX 06-JUN-1995; 95US-0471791.
XX
XX 16-SEP-1991; 91US-0762762.
XX
XX 16-MAR-1990; 90US-0494106.
PR

PR 13-AUG-1990; 90US-0567373.
PR 14-NOV-1990; 90US-0615784.
PR 14-MAR-1991; 91MO-USO1746.
PR 06-JUN-1995; 95US-0471791.
XX
XX (CALT) CALGENE INC.
XX
XX Knaut VC, Thompson GA;
XX
XX WPI: 1998-178544/16.
XX
XX N-PSDB: AAV15252.
DR
PT DNA encoding plant delta-9 desaturase protein - having amino acid
PT sequence of Carthamus tinctorius desaturase, useful for, e.g.
PT producing oil-seeds with modified levels of fatty acid saturation
XX
XX
XX Claim 7; Column 59-60; 87pp; English.
XX
XX The present sequence represents a Ricinus communis desaturase from
XX clone pCGN3230. The present invention describes a recombinant DNA
XX construct comprising a DNA sequence encoding a plant Delta-9 desaturase
XX protein. The present invention also provides a method of modifying fatty
XX acid composition in a host plant cell from a given fatty acid saturation
XX to a different fatty acid saturation, comprising growing a host plant
XX cell containing a recombinant DNA sequence which encodes a plant
XX desaturase under the control of regulatory elements functional in the
XX plant cell during lipid accumulation. Also, oilseeds having a modified
XX level of fatty acid saturation and oils produced from such oilseeds.
XX
XX Sequence 396 AA:
SQ
Query Match 72.3%; Score 1490; DB 19; Length 396;
Best Local Similarity 71.1%; Pred. No. 1.7e-134;
Matches 286; Conservative 50; Mismatches 52; Indels 14; Gaps 5;
OY 1 MALKLN-FOCKKNHPAFAKSPLEPTRVSSPVRVFASTVNSNSVLDNLKSP-----PN 53
DB 1 MALKLNFLSQTKLPSPALPMASTR--SPRFYMASTLKSQSKVEVNLKPFMPREVN 58
OY 54 LOYTHSMPPQKLEIFKSLDDMARNNVLIHLKSVKSWQPODYLPDVSDFGEQVRLE 113
DB 59 VOYTHSMPPQKLEIFKSLDDMARNNVLIHLKSVKSWQPODYLPDVSDFGEQVRLE 118
OY 114 RAKELIPDDYFVVLVGMITEEALPTYMSMLNRCQDKDETGAEPSSAMWTRAMTAENR 173
DB 119 RAKELIPDDYFVVLVGMITEEALPTYMSMLNRCQDKDETGAEPSSAMWTRAMTAENR 178
OY 174 HGDLNKLKYLISGRVDMRKIEKTIOYLIGSGMDIKSENSPYLGFIYTSFOERATFISHAN 233
DB 179 HGDLNKLKYLISGRVDMRKIEKTIOYLIGSGMDIKSENSPYLGFIYTSFOERATFISHAN 238
OY 234 TAKLAOHYGDKNIAHIGSIASDEKRHAATYKIVEKLAIEDPTTVIAFADMMRKKTIM 293
DB 239 TARQAKHEGDIKLAQICGIIADEKRHAATYKIVEKLAIEDPTTVIAFADMMRKKTIM 298
OY 294 PAHLMYDGSDELFEKHFETAQORVXYYSALDYCDILEFLVDKNVVERLTGLSDEGRAOE 353
DB 299 PAHLMYDGSDELFEKHFETAQORVXYYSALDYCDILEFLVDKNVVERLTGLSDEGRAOE 358
OY 354 YVCCELGPKIRVEEKVQGEKKKKAHP--VSFSWTFNRRLKI 394
DB 359 YVCCELGPKIRVEEKVQGEKKKKAHP--VSFSWTFNRRLKI 396
RESULT 3
AAR14189 standard; Protein: 396 AA.
ID AAR14189
XX
XX AAR14189:
XX
XX 11-DEC-1991 (first entry)
XX
XX R. communis delta9 desaturase from pCGN3230.
DE


```

XX Desaturase; fatty acid; saturation; chill tolerance; lipid;
KM herbicide.
XX Ricinus communis.
OS
PN MO9113972-A.
XX
PD 19-SEP-1991.
XX
PF 14-MAR-1991; 91WO-UO01746.
XX
PR 14-NOV-1990; 90US-0615784.
PR 16-MAR-1990; 90US-0494106.
PR 13-AUG-1990; 90US-0367373.
XX
PA (CALG-) CALGENE INC.
XX
PI Thompson G, Knauf V;
XX
DR WPI; 1991-295627/40.
DR N-PSDB; AAQ13964.
XX
PT DNA encoding a plant desaturase - used for modifying the satd.
PT fatty acid compsn. of plant cells and plant seeds
XX
PS Disclosure; Fig 3B; 128pp; English.
XX
CC Modification of fatty acid in a plant host cell to a different
CC percentage of fatty acid satn. is possible by growing a host plant
CC cell having integrated into its genome a recombinant DNA sequence
CC encoding this protein, under the control of regulatory elements
CC functional in the plant cell during lipid accumulation, under
CC conditions which will promote the activity of the regulatory elements.
CC By increasing the amt. of desaturase available in plant cells, an
CC increased percentage of unsatd. fatty acids may be provided, using
CC anti-sense technology, the amt. of desaturase can be decreased,
CC resulting in a higher percentage of fatty acids.
CC Using the desaturase gene and derivs. in cells and plants,
CC desirable traits such as chill tolerance may be introduced and
CC environmentally safe herbicide prods. may be provided.
CC See also AAQ13963-69.
XX
SQ Sequence 396 AA;
Query Match 71.8%; Score 1480; DB 12; Length 396;
Best local similarity 70.6%; Pred. No. 1.5e-133;
Matches 284; Conservative 51; Mismatches 53; Indels 14; Gaps 5;
OY 1 MALKLN-FQCKKNHRAAKSPLEPTRVSSPRVMASTVNSMWLDNLKSP-----PN 53
DB 1 MALKNPPLSQTKLPSPALPPMASTR--SPKFMVASTLKSGKEVENKKPFMPREYH 58
OY 54 LQVHSMSPQKLEIFKSLDDMRNNVLHLKSVKSMQODLPPDVSQGFPEQVRELRE 113
DB 59 VQVHSMSPQKLEIFKSLDDMRNNVLHLKSVKSMQODLPPDVSQGFPEQVRELRE 118
OY 114 RAKEIPDDYFVVLVGDMTTEALPTVMSMLNRCDSIKDETGAEPSSAMAMTATWAEENR 173
DB 119 RAKEIPDDYFVVLVGDMTTEALPTVMSMLNRCDSIKDETGAEPSSAMAMTATWAEENR 178
OY 174 HGDLINKLTVLSGRVDMRKIEKTIQYLLIGSGMDISENSPYLGFIYTSFOERATFISHAN 233
DB 179 HGDLINKLTVLSGRVDMRKIEKTIQYLLIGSGMDISENSPYLGFIYTSFOERATFISHAN 236
OY 234 TAKLAQHGDKNLAIHGSIASDEKRHATATYKIVKIEKLAETDPTTYIAFADMMRKIKM 293
DB 239 TAKQAKGKDKLADICGIIADDEKRHEATATYKIVKIEKLEIDPDGVLAFADMMRKIKM 298
OY 294 PAHLMYDGSDELLFKHTAVAVQRYVYSALDYCDLLEFLVDMWNERLGLSGDEGRKAOE 353
DB 299 PAHLMYDGRDQMLFDFHSAVAGRLGVYTAQDVADLLEFLVGMKMKDKLGLSAGQKAD 358

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OY 354 YVCELGPKTRVEEKVQKREKKKAEHP-VSPSWIFNREIKI 394
DB 359 YVCELRPEIRIRLQERAOGRAK----EAPTPFSPWIFDQVKL 396
RESULT 4
AAB48199
ID AAB48199 standard; Protein; 363 AA.
XX
AC AAB48199;
XX
DT 02-APR-2001 (first entry)
XX
DE Mature castor enzyme.
XX
KM Castor; delta9-18:0-acyl carrier protein desaturase; ACP; enzyme;
KM vegetable oil; fatty acid; nutrition; plant oil; mutant.
XX
OS Ricinus communis.
XX
FH Key Location/Qualifiers
FH FT Misc-difference 114
FH FT /note= "can be substituted by Ala"
FH FT Misc-difference 117
FH FT /note= "can be substituted by Arg"
FH FT Misc-difference 118
FH FT /note= "can be substituted by Gly"
FH FT Misc-difference 179
FH FT /note= "can be substituted by Val"
FH FT Misc-difference 181
FH FT /note= "can be substituted by Val"
FH FT Misc-difference 188
FH FT /note= "can be substituted by Leu"
PD MO200075170-A1.
PD 14-DEC-2000.
PF 08-JUN-2000; 2000MO-US15741.
PF 09-JUN-1999; 99US-0328550.
PR (BROO-) BROOKHAVEN SCI ASSOC LLC.
PA
XX
PI Shanklin J;
PI
DR WPI; 2001-091202/10.
DR N-PSDB; AAC84531.
XX
PT New mutant castor Delta9-18:0-Acyl Carrier Protein desaturase, useful
PT in producing commercially valuable products, e.g. vegetable oils useful
PT in human nutrition or as industrial chemicals
XX
PS Examples; Fig 1; 53pp; English.
XX
CC The invention relates to a new mutant castor Delta9-18:0-acyl carrier
CC protein (ACP) desaturase that has one or more amino acid substitutions
CC selected from: (a) Ala for Met at residue 114; (b) Arg for Thr at residue
CC 117; (c) Gly for Leu at residue 118; (d) Val for Pro at residue 179; (e)
CC Val for Thr at residue 181; (f) Leu for Gly at residue 186; and (g) Phe
CC for Thr at residue 181. The mutant castor Delta9-18:0-ACP desaturase is
CC useful in producing commercially useful products, such as vegetable oils
CC rich in monounsaturated fatty acids. Such vegetable oils are important in
CC human nutrition and can be used as renewable sources of industrial
CC chemicals. A method for specifically altering a function of a protein
CC through directed mutagenesis is also provided. The method can be used
CC altering enzymatic functions, binding functions or structural functions
CC of the castor desaturase enzyme. The method is also useful for
CC manipulating the physical properties and commercial uses of conventional
CC plant oils. The present sequence represents the mature castor enzyme.
XX
SQ Sequence 363 AA;

```


PA (DUPQ) DU PONT DE NEMOURS & CO E I.
 XX
 PI Hitz WD, Perez-Grau L, Yadav NS;
 XX
 DR WPI: 1998-332247/29.
 DR N-PSDB; AAV29236.
 XX
 PY Nucleic acids encoding soybean seed stearyl-ACP desaturase enzyme -
 PT are useful for the anti-sense inhibition of the enzyme in
 PT transformed plant cells
 XX
 PS Disclosure: Column 43-46; 26pp; English.
 XX
 CC This is the amino acid sequence of soybean stearyl ACP-desaturase,
 CC used in the method of the invention, which involves the creation of
 CC chimeric genes which are used in (antisense orientation) to transform
 CC plant cells. The nucleic acids are useful for controlling the levels
 CC of (un)saturated fatty acids in soybean oil. In transformed cells
 CC (seeds), the chimeric genes transcribe the antisense RNA to the
 CC complementary mRNA for the enzyme. This results in inhibition of
 CC expression of the endogenous enzyme and reduction in desaturation of
 CC seed oil. This results in seed oil which is low in saturates and
 CC polyunsaturates and high in monosaturates, giving an oil which is
 CC healthier.
 CC
 XX
 SQ Sequence 391 AA;
 Query Match 69.7%; Score 1436.5; DB 19; Length 391;
 Best Local Similarity 68.5%; Pred. No. 2.3e-129; Indels 31; Gaps 4;
 Matches 278; Conservative 44; Mismatches 53;
 QY 1 MALKLNFOCKRNHPAFAKSPLPVTRVS-----SPRVFASTVNSNSMVLNLIKSP- 51
 DB 1 MALRLN-----PIPTQTFSLPQMPSLRSPFRMASTRSGSKKEVENIKRPF 46
 QY 52 -----PNQVTHSMPPQKLEIFKSLDDMAANNVLIHLSVEKSWOPDYLPDPVSGEPE 106
 DB 47 TPPEVHVQVTHSMPPQKLEIFKSLDDMAANNVLIHLSVEKSWOPDYLPDPVSGEPE 106
 QY 107 QVRELREKAKEIPDDYFVVLVGDMTTEALPTYMSMLNRCDCIKDETGAEPSSAMAMWTRA 166
 DB 107 QVRELREKAKEIPDDYFVVLVGDMTTEALPTYMSMLNRCDCIKDETGAEPSSAMAMWTRA 166
 QY 167 WTAENRHRGDLNKLKLYLSGRVDMRKIEKTIQYLIGSGMDISENSPYLGFTYTSFOERA 226
 DB 167 WTAENRHRGDLNKLKLYLSGRVDMRKIEKTIQYLIGSGMDISENSPYLGFTYTSFOERA 226
 QY 227 TFIISANPAKLAQHYGDKNLAHIGSISASDEKRHATAYTKIVEKLAIEDPDTVIAFADM 286
 DB 227 TFIISGNTARLAKHEGDIKQICQMSIASDEKRHETAYTKIVEKLEFVDPDGTVMAFADM 286
 QY 287 MRKKTTPAHMLMYDGSDELLEFHFPAVAQRYVYSALDYCDILEFLVDKWNVERLTGLSD 346
 DB 287 MRKKTTPAHMLMYDGRDLEFDNYSVAQRIQVYAKDYADILEFLVGKWKVEQLTGLSG 346
 QY 347 EGRKAQEVYCELGPRIKTRVEEKVQKEKKKAHPYSPFSMIREL 392
 DB 347 EGRKAQEVYCELGPRIKTRVEEKVQKEKKKAHPYSPFSMIREL 392
 RESULT 7
 AAR14188 ID AAR14188 standard; Protein; 396 AA.
 XX
 AC AAR14188;
 XX
 DT 11-DEC-1991 (first entry)
 XX
 DE C. tinctorius delta9 desaturase from pCGN274.
 XX
 KW Desaturase; fatty acid; saturation; chill tolerance; lipid;
 XX herbicide.
 XX

OS Carthamus tinctorius.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..33
 FT /label= transit_peptide
 FT Protein 34..396
 FT /label= mature_protein
 XX
 XX MO9113972-A.
 XX
 PD 19-SEP-1991.
 XX
 XX 14-MAR-1991; 91WO-0001746.
 XX
 PF 14-NOV-1990; 90US-0615784.
 PR 16-MAR-1990; 90US-0494106.
 PR 13-AUG-1990; 90US-0567373.
 XX
 XX (CALG-) CALGENE INC.
 PA
 PI Thompson G, Knauf V;
 XX
 XX WPI: 1991-295627/40.
 DR N-PSDB; AAQ13963.
 XX
 PT DNA encoding a plant desaturase - used for modifying the satd.
 PT fatty acid compsn. of plant cells and plant seeds
 PS Disclosure: Fig 2; 128pp; English.
 XX
 CC Modification of fatty acid in a plant host cell to a different
 CC percentage of fatty acid satn. is possible by growing a host plant
 CC cell having integrated into its genome a recombinant DNA sequence
 CC encoding this protein, under the control of regulatory elements
 CC functional in the plant cell during lipid accumulation, under
 CC conditions which will promote the activity of the regulatory elements.
 CC By increasing the amt. of desaturase available in plant cells, an
 CC increased percentage of unsatd. fatty acids may be provided, using
 CC anti-sense technology, the amt. of desaturase can be decreased,
 CC resulting in a higher percentage of fatty acids.
 CC using the desaturase gene and derivs. in cells and plants,
 CC desirable traits such as chill tolerance may be introduced and
 CC environmentally safe herbicide prods. may be provided.
 CC See also AAQ13963-69.
 CC
 XX
 SQ Sequence 396 AA;
 Query Match 68.2%; Score 1406; DB 12; Length 396;
 Best Local Similarity 67.1%; Pred. No. 2e-126;
 Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;
 QY 1 MALKL---NNOCKRNHPAFAKSPLPVTRVSPPRVFASTVNSNSMVLNLIKSP----- 51
 DB 1 MALRLFPVLYQSEKYSFSPK-----ANLRSPFAASTLGSTPVDNAKKRFPQPRE 56
 QY 52 PNQVTHSMPPQKLEIFKSLDDMAANNVLIHLSVEKSWOPDYLPDPVSGEPEQYREL 111
 DB 57 VHQVTHSMPPQKLEIFKSLDDMAANNVLIHLSVEKSWOPDYLPDPVSGEPEQYREL 116
 QY 112 REKAKEIPDDYFVVLVGDMTTEALPTYMSMLNRCDCIKDETGAEPSSAMAMWTRAFAE 171
 DB 117 RARAKEIPDDYFVVLVGDMTTEALPTYMSMLNRCDCIKDETGAEPSSAMAMWTRAFAE 176
 QY 172 NRRGDLNKLKLYLSGRVDMRKIEKTIQYLIGSGMDISENSPYLGFTYTSFOERATFISH 231
 DB 177 NRRGDLNKLKLYLSGRVDMRKIEKTIQYLIGSGMDISENSPYLGFTYTSFOERATFISH 236
 QY 232 ANPAKLAQHYGDKNLAHIGSISASDEKRHATAYTKIVEKLAIEDPDTVIAFADMRRKI 291
 DB 237 GNTARHAKKHGDVYKLAIGTIGSIASDEKRHETAYTKIVEKLEFIDPDGTVALAFADMRRKI 296
 QY 292 TMRPAHMLMYDGSDELLEFHFPAVAQRYVYSALDYCDILEFLVDKWNVERLTGLSDEGRKA 351
 :||||||| : :||:||||| :||: || ||||| :| ||||| |||||

[illegible][illegible]

QY 52 PNLQVTHSMPPQKLEIFKSLSDMARNNLVLIHKSVKSWQPDYLPDPVSDGFEEQYREL 111
DQ 57 VHVQVTHSMPPQKLEIFKSLSDMARNNLVLIHKSVKSWQPDYLPDPVSDGFEEQYREL 116
QY 112 REBAKEIPDDYFVVLVGMITEEALPTYSMLNRCDCIKDETGAEPSSAMMTTAAWTAEE 171
DQ 117 RARAKEIPDDYFVVLVGMITEEALPTYSMLNRCDCIKDETGAEPSSAMMTTAAWTAEE 176
QY 172 NRHGDLLKTYLISGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFITYTSFOERATFVSH 231
DQ 177 NRHGDLLKTYLISGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFITYTSFOERATFVSH 236
QY 232 ANTAKLAQHYGDKNLAIHICGSIASDEKRRHATYTKIVEKLAIEDPDTVTIAFADMMARKKI 291
DQ 237 GNTARHAKHDGVKLAQICGTIASDEKRRHATYTKIVEKLAIEDPDTVTIAFADMMARKKI 296
QY 292 TMRPAHLMYDGSDELLEFKHFTAVAAQRYVYSALDYCDILEFLVDKNVVERLTGSLGDEGRKA 351
DQ 297 SMPAHLMYDGRDNDLFEHFSAAVQRLGYTTAKDYADILEFLVGRMKVADLTGLSGEGRKA 356
QY 352 QEYVCELGPRIKRVEEKVQGEKKKKAEPH-VSPSMIFNRELKI 394
DQ 357 QDYVCGLPRIKRLERAAQGRK---EGPVVPFSWIFPDQVKL 396

RESULT 10
AAM44349
ID AAM44349 standard; Protein: 396 AA.
XX AAM44349;
AC AAM44349;
XX 28-MAY-1998 (first entry)
DT 28-MAY-1998 (first entry)
XX Carthamus tinctorius desaturase from clone pCGN2754.
DE Carthamus tinctorius; safflower; delta-9 desaturase; oilseed;
XX Carthamus tinctorius; safflower; delta-9 desaturase; oilseed;
KW fatty acid saturation.
KM Carthamus tinctorius.
OS Carthamus tinctorius.
XX
FH Key Location/Qualifiers
FT Peptide 1..33
FT Protein /label= signal
FT Protein 34..396
FT Protein /label= desaturase
XX
XX US5723595-A.
XX 03-MAR-1998.
PD 03-MAR-1998.
XX
PF 06-JUN-1995; 95US-0471791.
XX
XX 16-SEP-1991; 91US-0762762.
PR 16-MAR-1990; 90US-0494106.
PR 13-AUG-1990; 90US-0567373.
PR 14-NOV-1990; 90US-0615784.
PR 14-MAR-1991; 91MO-US01746.
PR 06-JUN-1995; 95US-0471791.
XX
PA (CALJ) CALGENE INC.
XX
XX Knauf VC, Thompson GA;
PI WPI: 1998-178544/16.
XX N-PSDB; AAV15250.
DR
XX DNA encoding plant delta-9 desaturase protein - having amino acid
PT sequence of Carthamus tinctorius desaturase, useful for, e.g.
PT producing oil-seeds with modified levels of fatty acid saturation
XX
PS Claim 5; Column 53-56; 87pp; English.
XX
CC The present sequence represents a Carthamus tinctorius desaturase from

CC clone pCGN2754. The present invention describes a recombinant DNA
CC construct comprising a DNA sequence encoding a plant delta-9 desaturase
CC protein. The present invention also provides a method of modifying fatty
CC acid composition in a host plant cell from a given fatty acid saturation
CC to a different fatty acid saturation, comprising growing a host plant
CC cell containing a recombinant DNA sequence which encodes a plant
CC desaturase under the control of regulatory elements functional in the
CC plant cell during lipid accumulation. Also, oilseeds having a modified
CC level of fatty acid saturation and oils produced from such oilseeds.
XX
SQ Sequence 396 AA;

Query Match 68.2%; Score 1406; DB 19; Length 396;
Best Local Similarity 67.1%; Pred. No. 2e-126;
Matches 271; Conservative 54; Mismatches 61; Indels 18; Gaps 5;

QY 1 MALKL---NQCKKNHFAFAKSPFLPYTRSSPPVMASTYNSMWLDNFKSP----- 51
DQ 1 MALKLFPVTLQSEKYSFSPKK---ANLRSPKFAVASTIGSTPYVDNAKKKFPQPRE 56
QY 52 PNLQVTHSMPPQKLEIFKSLSDMARNNLVLIHKSVKSWQPDYLPDPVSDGFEEQYREL 111
DQ 57 VHVQVTHSMPPQKLEIFKSLSDMARNNLVLIHKSVKSWQPDYLPDPVSDGFEEQYREL 116
QY 112 REBAKEIPDDYFVVLVGMITEEALPTYSMLNRCDCIKDETGAEPSSAMMTTAAWTAEE 171
DQ 117 RARAKEIPDDYFVVLVGMITEEALPTYSMLNRCDCIKDETGAEPSSAMMTTAAWTAEE 176
QY 172 NRHGDLLKTYLISGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFITYTSFOERATFVSH 231
DQ 177 NRHGDLLKTYLISGRVDMRKIEKTIQYLLIGSGMDIKSENSPYLGFITYTSFOERATFVSH 236
QY 232 ANTAKLAQHYGDKNLAIHICGSIASDEKRRHATYTKIVEKLAIEDPDTVTIAFADMMARKKI 291
DQ 237 GNTARHAKHDGVKLAQICGTIASDEKRRHATYTKIVEKLAIEDPDTVTIAFADMMARKKI 296
QY 292 TMRPAHLMYDGSDELLEFKHFTAVAAQRYVYSALDYCDILEFLVDKNVVERLTGSLGDEGRKA 351
DQ 297 SMPAHLMYDGRDNDLFEHFSAAVQRLGYTTAKDYADILEFLVGRMKVADLTGLSGEGRKA 356
QY 352 QEYVCELGPRIKRVEEKVQGEKKKKAEPH-VSPSMIFNRELKI 394
DQ 357 QDYVCGLPRIKRLERAAQGRK---EGPVVPFSWIFPDQVKL 396

RESULT 11
AAR82024
ID AAR82024 standard; Protein: 391 AA.
XX AAR82024;
AC AAR82024;
XX
DT 10-APR-1996 (first entry)
XX
XX Stearoyl-ACP-desaturase precursor.
DE Stearoyl-ACP-desaturase precursor.
XX
KW Stearoyl-ACP-desaturase; soybean; seed oil; vegetable oil;
KW fatty acid; stearic acid; transgenic plant; crop improvement.
XX
XX Glycine max cv. Wye.
OS
FH Key Location/Qualifiers
FT Peptide 1..32
FT Protein /label= Transil_peptide
FT Protein 33..391
FT Protein /label= Mat_protein
XX
XX US5443974-A.
XX
XX 22-APR-1995.
PD 22-APR-1995.
XX
PF 25-MAY-1990; 90US-0529049.
XX
XX 11-DEC-1992; 92US-0995657.
PR

```

PR 25-MAY-1990; 9005-0529049.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
XX Hiltz WD, Perez-Grau L, Yadav NS;
XX
XX WPI: 1995-302121/39.
XX
XX N-PSDB: AAT00395.
XX
XX New isolated soybean stearyl-ACP desaturase gene - use for the
XX prodn. of seed oil contg. altered levels of satd. and unsatd. fatty
XX acids
XX
XX Disclousure; Column 41-44; 25pp; English.
XX
XX The stearyl-ACP-desaturase precursor (AAR82024) is the product of
XX a cDNA clone (AAT00395) derived from soybean developing leaves. It
XX catalyses the conversion of stearyl-ACP to oleoyl-ACP.
XX Expression of the mature enzyme in transgenic plants such as soybean,
XX rapeseed, sunflower, cocoa, peanut, sunflower and corn, allows the
XX fatty acid composition, esp. the stearic acid content, of the seed oil
XX to be controlled.
XX
XX Sequence 391 AA:
SQ
Query Match 68.1%; Score 1404.5; DB 16; Length 391;
Best Local Similarity 67.5%; Pred. No. 2.7e-126;
Matches 274; Conservative 45; Mismatches 56; Indels 31; Gaps 4;
QY 1 MALKLNFOCKKNNHFAFAKSPLPVTRVS-----SPRVEMASTVNSNVLNKLKSP- 51
DB 1 MALRLN-----PIPTQTFSLPQMPSLRSPFRMASTLRSKKEVENIKRPF 46
QY 52 -----PMLQVTHSMPPOKLEIFKSLDMDARNVLIHLKSVKSNOPQDYLDPVSDGFEE 106
DB 47 TPPEHVAVQYTHSMPPOKLEIFKSLDMDARNVLIHLKSVKSNOPQDYLDPVSDGFEE 106
QY 107 QVRLRRARKEIPDDYFVVLVGDMLTEALPTVMSMLNRCDGKDEGAEPSSAMAMWTRA 166
DB 107 QVRLRRARKEITLYYFVLVGDMLTEALPTVMTLNTLDGVRDETCASLSMAIWTRA 166
QY 167 WTAENRHGDLINKLYLSGRVDMRKIEKTQYLLIGSGMDIKSENSPYLGFIYTSFOERA 226
DB 167 WTAENRHGDLINKLYLSGRVDMRKIEKTQYLLIGSGMDIKSENSPYLGFIYTSFOERA 226
QY 227 TFLSHANTAKLAOHYGOKNLAHICGSIASDEKRHATAYTKIYEKLAIEDPTTIAFADM 286
DB 227 TFLSHGNTARLAKERHGDIKLAQICGMILASDEKRHETATTKIYEKLFYVDPDQTVAAFD 286
QY 287 MRKKITMPAHILMYDGSDELLFKHFTAVAQRYVYSALDYCDILEFLVDKMWVERLTGLSD 346
DB 287 MRKKITMPAHILMYDGRDNLFDNYSAVAQRIQVYAKDYADILEFLVGRKWEQVLEGLSG 346
QY 347 EGRAQAEYVCELGPKITRVEEKYQGEKKKAHHPVSFSWIFNREL 392
DB 347 EGRAQAEYVCGLPKITRLEERAQAKGKESST--LKFSTWIDREV 389

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RESULT 12

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AAW14797
ID AAW14797 standard; Protein: 401 AA.
XX
XX AAW14797:
AC
AC AAW14797 (first entry)
DT
DT 03-JUL-1997
XX
XX Rapeseed stearyl-ACP desaturase BND11.
XX
XX Stearoyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;
XX anisense; triglyceride; stearic acid; transgenic plant; oilseed;
XX vegetable oil; mangosteen; Garcinia mangifera.
XX
XX Brassica napus cv. 212/86.
OS

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XX
XX W09712047-A1.
XX
XX 03-APR-1997.
XX
XX 30-SEP-1996; 96WO-US16078.
XX
XX 29-SEP-1995; 95US-0537083.
XX
XX (CALJ) CALGENE INC.
XX
XX Knauf VC, Kridl J, Lassner MW;
XX
XX WPI: 1997-212906/19.
XX
XX N-PSDB: AAT63437.
XX
XX Increasing levels of stearate in plant seed triglyceride(s) -
XX using a DNA sequence encoding acyl-ACP thioesterase protein having
XX substantial activity on C18:0 acyl-ACP substrates
XX
XX Example 5; Fig6A-6C; 55pp; English.
XX
XX Oilseed rape stearyl-ACP desaturases BND11 (AAW14797) and BND9
XX (AAW14798) each catalyse the desaturation of stearyl-ACP (C18:0) to
XX oleoyl-ACP (C18:1). Their amino acid sequences were deduced from
XX cDNA clones (AAT63437-38) isolated from a Brassica napus cv. 212/86
XX mid-mutation seed cDNA library. An antisense gene was constructed
XX to generate antisense RNA homologous to both BND9 and BND11. In
XX transgenic Brassica plants expressing the stearyl-ACP desaturase
XX antisense construct and mangosteen Class I acyl-ACP thioesterase
XX Garmfalai (see also AAW14795), levels of C18:0 in the seed oil may
XX exceed 50% of total fatty acids.
XX
XX Sequence 401 AA:
SQ
Query Match 67.9%; Score 1400.5; DB 18; Length 401;
Best Local Similarity 65.4%; Pred. No. 6.9e-126;
Matches 265; Conservative 67; Mismatches 58; Indels 15; Gaps 5;
QY 1 MALKLNFOCKKNNHFAFAKSPLPVTRVSPP-VEFMST-----VNSNVLNKLKSP----- 51
DB 1 MALKLNPLASQYKPLPSSARP-PISTLRSPKFLCLASSSPALSSSTKKEVESLKKPFPP 59
QY 52 --PMLQVTHSMPPOKLEIFKSLDMDARNVLIHLKSVKSNOPQDYLDPVSDGFEEQYR 109
DB 60 KEVHVOVLSHMPPOKLEIFKSMEDWAEHNLPLKDVESKSNOPQDYLDPASDGFEDQYK 119
QY 110 ELRERARKEIPDDYFVVLVGDMLTEALPTVMSMLNRCDGKDEGAEPSSAMAMWTRA 169
DB 110 ELRERARKEIPDDYFVVLVGDMLTEALPTVMTLNTLDGVRDETCASLSMAIWTRA 179
QY 170 EENRHGDLINKLYLSGRVDMRKIEKTQYLLIGSGMDIKSENSPYLGFIYTSFOERATF 229
DB 170 EENRHGDLINKLYLSGRVDMRKIEKTQYLLIGSGMDIKSENSPYLGFIYTSFOERATF 229
QY 229 TFLSHANTAKLAOHYGOKNLAHICGSIASDEKRHATAYTKIYEKLAIEDPTTIAFADM 289
DB 229 TFLSHGNTARLAKERHGDIKLAQICGMILASDEKRHETATTKIYEKLFYVDPDQTVAAFD 289
QY 289 SHANTAKLAOHYGOKNLAHICGSIASDEKRHATAYTKIYEKLAIEDPTTIAFADM 349
DB 289 SHANTAKLAOHYGOKNLAHICGSIASDEKRHETATTKIYEKLFYVDPDQTVAAFD 349
QY 349 KITMPAHILMYDGSDELLFKHFTAVAQRYVYSALDYCDILEFLVDKMWVERLTGLSDGR 392
DB 349 KITMPAHILMYDGRDNLFDNYSAVAQRIQVYAKDYADILEFLVGRKWEQVLEGLSG 392
QY 392 KAOEYVCELGPKITRVEEKYQGEKKKAHHPVSFSWIFNREL 394
DB 360 KAOEYVCELGPKITRLEERAQAKKGP--KIPFSWIDREV 401

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RESULT 13

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AAW14190
ID AAW14190 standard; Protein: 398 AA.
XX
XX AAW14190:
AC

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XX 11-DEC-1991 (first entry)
XX B. campestris delta9 desaturase from PCGN3235.
XX Desaturase; fatty acid; saturation; chill tolerance; lipid;
XX herbicide.
XX Brassica campestris.
XX OS
XX MO9113972-A.
XX PN
XX 19-SEP-1991.
XX PD
XX 14-MAR-1991; 91WO-U001746.
XX PE
XX 14-NOV-1990; 90US-0615784.
XX PR 16-MAR-1990; 90US-0494106.
XX PR 13-AUG-1990; 90US-0567373.
XX PA
XX (CALG-) CALGENE INC.
XX PI Thompson G, Knauf V;
XX XX
XX WPI: 1991-295627/40.
XX DR N-PSDB; AAQ13965.
XX XX
XX DNA encoding a plant desaturase - used for modifying the satd.
XX PT fatty acid compsn. of plant cells and plant seeds
XX XX
XX Disclosure: Fig 4C; 128bp; English.
XX XX
XX Modification of fatty acid in a plant host cell to a different
XX percentage of fatty acid satn. is possible by growing a host plant
XX cell having integrated into its genome a recombinant DNA sequence
XX encoding this protein, under the control of regulatory elements
XX functional in the plant cell during lipid accumulation, under
XX conditions which will promote the activity of the regulatory elements.
XX CC By increasing the amt. of desaturase available in plant cells, an
XX CC increased percentage of unsatd. fatty acids may be provided, using
XX CC anti-sense technology, the amt. of desaturase can be decreased,
XX CC resulting in a higher percentage of fatty acids.
XX CC Using the desaturase gene and derivs. in cells and plants,
XX CC desirable traits such as chill tolerance may be introduced and
XX CC environmentally safe herbicide prods. may be provided.
XX CC See also AAQ13963-69.
XX XX
XX Sequence 398 AA:
XX
XX Query Match 67.7%; Score 1396; DB 12; Length 398;
XX Best Local Similarity 66.9%; Pred. NO. 1.8e-125;
XX Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;
XX
QY 1 MALKLNFOCKR--NHPAFAKSPPLVTRVSSPRVEMASTVNSNVLNLSKSP-----P 52
QY 1 MALKLNPLASOPYNPPSS-ARPPSTFRSPKFLCLASSSPALSSKEVESLKKFPPTPKREV 59
DB 1 MALKLNPLASOPYNPPSS-ARPPSTFRSPKFLCLASSSPALSSKEVESLKKFPPTPKREV 59
XX
QY 53 NLOVTHSMPPOKLEIFKSLDDMARNNVLIHLKSVKSMQPODYLPPVSDGFEEOVRELR 112
QY 60 HVOYLHSMPPOKLEIFKSMEDMAEQNLTLQKDVESKMQPODLPPASDGFEDQVRELR 119
DB 60 HVOYLHSMPPOKLEIFKSMEDMAEQNLTLQKDVESKMQPODLPPASDGFEDQVRELR 119
XX
QY 113 ERAKEIPDDYFVVLVGMITEALPTYSMLNRCIDKIDETGAEPASAMMTRAWTAEN 172
QY 120 ERARELPPDYFVVLVGMITEALPTYOFTMLNTLDGVRDETGAESPISMAIWTAWTAEN 179
DB 120 ERARELPPDYFVVLVGMITEALPTYOFTMLNTLDGVRDETGAESPISMAIWTAWTAEN 179
XX
QY 173 RHGDLNLKTYLISGVNDAKKIKETIOYLIGSGMDIKSENSPYIGITYTSFOERATFISHA 232
QY 180 RHGDLNLKTYLISGVNDAKKIKETIOYLIGSGMDIPRTENNPPYIGITYTSFOERATFISHG 239
DB 180 RHGDLNLKTYLISGVNDAKKIKETIOYLIGSGMDIPRTENNPPYIGITYTSFOERATFISHG 239
XX
QY 233 NTAKLAOHYGDKNLHIGSGIASDEKRNATATYTKIETKLAETDPPDTYVAFAMMRKITF 292
QY 240 NTARBAKEHGDCLKLQIGCTIAADEKRHETATYTKIETKLEIDPDGCTVMAFAMMRKITIS 299
DB 240 NTARBAKEHGDCLKLQIGCTIAADEKRHETATYTKIETKLEIDPDGCTVMAFAMMRKITIS 299

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QY 293 MPAHLMTDGSDELLFKHFTAVAQRVXYISALDYCDILEFLVDKMNVERLTGSDGKRAQ 352
QY 300 MPAHLMTDGRDESLFDNFSSVQAQRLGYTAKDYADILEFLVGRMKIESLTGSGKNAQ 359
DB 300 MPAHLMTDGRDESLFDNFSSVQAQRLGYTAKDYADILEFLVGRMKIESLTGSGKNAQ 359
XX
QY 353 EYVCELGPKIRRVKEKVOGKEKKKAHPVSESMFNREIKI 394
QY 360 EYLCGLTPRIRLRIDERAQARAKGP--KVPFSWIHREVOL 398
DB 360 EYLCGLTPRIRLRIDERAQARAKGP--KVPFSWIHREVOL 398
XX
RESULT 14
AAW14798
ID AAW14798 standard; Protein: 398 AA.
XX
AC AAW14798;
XX
XX 03-JUL-1997 (first entry)
XX DT
XX DE Rapeseed stearyl-ACP desaturase BND9.
XX XX
XX Stearoyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;
XX KM antisenase; triglyceride; stearic acid; transgenic plant; oilseed;
XX KM vegetable oil; mangosteen; Garcinia mangifera.
XX XX
XX OS Brassica napus cv. 212/86.
XX XX
XX PN MO9712047-A1.
XX XX
XX PD 03-APR-1997.
XX XX
XX PE 30-SEP-1996; 96WO-US16078.
XX XX
XX PR 29-SEP-1995; 95US-0537083.
XX XX
XX PA (CALG ) CALGENE INC.
XX XX
XX PI Knauf VC, Kridl J, Lassner MW;
XX XX
XX DR WPI: 1997-212906/19.
XX XX
XX DR N-PSDB; AAT63438.
XX XX
XX PT Increasing levels of stearate in plant seed triglyceride(s) -
XX PT using a DNA sequence encoding acyl-ACP thioesterase protein having
XX PT substantial activity on C18:0 acyl-ACP substrates
XX XX
XX PS Example 5; Fig7A-7C; 55bp; English.
XX XX
XX CC Oilseed rape stearyl-ACP desaturases BND11 (AAW14797) and BND9
XX CC (AAW14798) each catalyze the desaturation of stearyl-ACP (C18:0) to
XX CC oleoyl-ACP (C18:1). Their amino acid sequences were deduced from
XX CC cDNA clones (AAT63437-38) isolated from a Brassica napus cv. 212/86
XX CC mid-mutation seed cDNA library. An antisenase gene was constructed
XX CC to generate antisenase RNA homologous to both BND9 and BND11. In
XX CC transgenic Brassica plants expressing the stearyl-ACP desaturase
XX CC antisenase construct and mangosteen Class I acyl-ACP thioesterase
XX CC GammaFata1 (see also AAW14795), levels of C18:0 in the seed oil may
XX CC exceed 50% of total fatty acids.
XX XX
XX Sequence 398 AA:
XX
XX Query Match 67.7%; Score 1396; DB 18; Length 398;
XX Best Local Similarity 66.9%; Pred. NO. 1.8e-125;
XX Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;
XX
QY 1 MALKLNFOCKR--NHPAFAKSPPLVTRVSSPR--VFMASTVNSNVLNLSKSP-----P 52
QY 1 MALKLNPLASOPYNPPSSAR-PVSTFRSPKFLCLASSSPALSSKEVESLKKFPPTPKREV 59
DB 1 MALKLNPLASOPYNPPSSAR-PVSTFRSPKFLCLASSSPALSSKEVESLKKFPPTPKREV 59
XX
QY 53 NLOVTHSMPPOKLEIFKSLDDMARNNVLIHLKSVKSMQPODYLPPVSDGFEEOVRELR 112
QY 60 HVOYLHSMPPOKLEIFKSMEDMAEQNLTLQKDVESKMQPODLPPASDGFEDQVRELR 119
DB 60 HVOYLHSMPPOKLEIFKSMEDMAEQNLTLQKDVESKMQPODLPPASDGFEDQVRELR 119
XX
QY 113 ERAKEIPDDYFVVLVGMITEALPTYSMLNRCIDKIDETGAEPASAMMTRAWTAEN 172
QY 113 ERAKEIPDDYFVVLVGMITEALPTYSMLNRCIDKIDETGAEPASAMMTRAWTAEN 172
DB 113 ERAKEIPDDYFVVLVGMITEALPTYSMLNRCIDKIDETGAEPASAMMTRAWTAEN 172

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Db 120 ERARELPDVFVVLVGDMTTEALPTVQTMNTLDGVRDEFGASPTSWAIVTRAWTAEN 179
 QY 173 RHGDLINKLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLFTYTSFOERATFISHA 232
 Db 180 RHGDLINKLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLFTYTSFOERATFISHG 239
 QY 233 NTAKLAOHYGDKNLAHICGSIASDEKRRHATATYTKIVEKLAIEDPDTTVIAPADMMRKIT 292
 Db 240 NTAKOAKHEGDLKLAQICGTIAADEKRHETATYTKIVEKLFEPIDPDGTVMAFADMMRKIS 299
 QY 293 MPAHLMYDGSDELLFKHFTAVAQRYVXSALDYCDILEFLYDKMNVRELTLGSDGGRKAQ 352
 Db 300 MPAHLMYDGRDESLFDNFSVAQRGLGYTAKDYADILEFLVGRWKIESLTGLSGGNKAQ 359
 QY 353 EYVCELGPKTRVVEKVOGKEKKKAHPVSFSWIFNRELKI 394
 Db 360 EYLGCLTPRIRRLDERAQAARKGP---KVPEFSWIHREVQL 398

RESULT 15

AAW44351 standard; Protein: 398 AA.

AAW44351:

28-MAY-1998 (first entry)

Brassica campestris desaturase from clone pCGN3235.

Brassica campestris; castor bean; delta-9 desaturase; oilseed;

fatty acid saturation.

Brassica campestris.

US5723595-A.

03-MAR-1998.

06-JUN-1995; 95US-0471791.

16-SEP-1991; 91US-0762762.

16-MAR-1990; 90US-0494106.

13-AUG-1990; 90US-0567373.

14-NOV-1990; 90US-0615784.

14-MAR-1991; 91WO-US01746.

06-JUN-1995; 95US-0471791.

(CALJ) CALGENE INC.

Knauf VC, Thompson GA;

MP1: 1998-178544/16.

N-PSDB; AAV15253.

Claim 9: Column 63-66; 87pp; English.

The present sequence represents a Brassica campestris desaturase from clone pCGN3235. The present invention describes a recombinant DNA construct comprising a DNA sequence encoding a plant Delta-9 desaturase protein. The present invention also provides a method of modifying fatty acid composition in a host plant cell from a given fatty acid saturation to a different fatty acid saturation, comprising growing a host plant cell containing a recombinant DNA sequence which encodes a plant desaturase under the control of regulatory elements functional in the plant cell during lipid accumulation. Also, oilseeds having a modified level of fatty acid saturation and oils produced from such oilseeds.

Sequence 398 AA;

Query Match 67.7%; Score 1396; DB 19; Length 398;
 Best Local Similarity 66.9%; Pred. No. 1.8e-125;
 Matches 269; Conservative 55; Mismatches 66; Indels 12; Gaps 4;

QY 1 MALKLNFOCKR--NHPAFAKSPPLVTRVSSPRVEMASTVNSNSWLDMLKSP-----P 52
 Db 1 MALKLNPLASQYNPPSS-ARPPISIFRSPKFLCLASSPALSSKVESLAKRPFTPPKEY 59
 QY 53 NIQVTHSNPPOKLETFKSLDDMARNNVLIHLKSVESKMPQDYLDPDVSDFGEQYREL 112
 Db 60 HVOVLSMPPOKTEIFKSMEDMAEONMLIQLDKVEKSMQPODFLPDPSDGFEDQYREL 119
 QY 113 ERAKEIPDDYFVVLVGDMTTEALPTVYMSMLNRCGIDKDETGAEPSAMAMWTAWTAEN 172
 Db 120 ERARELPDVFVVLVGDMTTEALPTVQTMNTLDGVRDEFGASPTSWAIVTRAWTAEN 179
 QY 173 RHGDLINKLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLFTYTSFOERATFISHA 232
 Db 180 RHGDLINKLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLFTYTSFOERATFISHG 239
 QY 233 NTAKLAOHYGDKNLAHICGSIASDEKRRHATATYTKIVEKLAIEDPDTTVIAPADMMRKIT 292
 Db 240 NTAKOAKHEGDLKLAQICGTIAADEKRHETATYTKIVEKLFEPIDPDGTVMAFADMMRKIS 299
 QY 293 MPAHLMYDGSDELLFKHFTAVAQRYVXSALDYCDILEFLYDKMNVRELTLGSDGGRKAQ 352
 Db 300 MPAHLMYDGRDESLFDNFSVAQRGLGYTAKDYADILEFLVGRWKIESLTGLSGGNKAQ 359
 QY 353 EYVCELGPKTRVVEKVOGKEKKKAHPVSFSWIFNRELKI 394
 Db 360 EYLGCLTPRIRRLDERAQAARKGP---KVPEFSWIHREVQL 398

Search completed: December 1, 2002, 21:20:14
 Job time : 41 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 1, 2002, 21:19:11 ; Search time 21 Seconds
(Without alignments)
1803.665 Million cell updates/sec

Title: US-09-732-597-2

Perfect score: 2062
Sequence: 1 MALKNFQCKKHPAAFAKS.....KKKAHPVSPSWIFNRELKI 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1545.5	75.0	385	2 A47245	acyl-[acyl-carrier
2	1490	72.3	396	1 OHCSAD	acyl-[acyl-carrier
3	1422.5	69.0	411	2 T07806	acyl-[acyl-carrier
4	1410.5	68.4	399	1 OHSPAD	acyl-[acyl-carrier
5	1408	68.3	396	2 B39170	acyl-[acyl-carrier
6	1406	68.2	396	2 A39173	acyl-[acyl-carrier
7	1396	67.7	398	2 S23351	acyl-[acyl-carrier
8	1395	67.7	396	2 T14264	acyl-[acyl-carrier
9	1386.5	67.2	393	2 S44202	acyl-[acyl-carrier
10	1386.5	67.2	399	2 S24955	acyl-[acyl-carrier
11	1385.5	67.2	393	2 T07653	acyl-[acyl-carrier
12	1381.5	67.0	401	2 E84869	stearyl-ACP desat
13	1381	67.0	396	2 T14268	acyl-[acyl-carrier
14	1375.5	66.7	397	2 T10793	acyl-[acyl-carrier
15	1352	65.6	396	2 T14172	acyl-[acyl-carrier
16	1347.5	65.3	407	2 S71264	acyl-[acyl-carrier
17	1320.5	64.0	394	2 T51494	stearyl-acyl carr
18	1310.5	63.6	390	2 T04097	acyl-[acyl-carrier
19	1246	60.4	396	2 S31959	acyl-[acyl-carrier
20	1223.5	59.3	401	2 T51493	stearyl-acyl carr
21	1197	58.1	374	2 A96502	probable acyl-acyl
22	295	14.3	328	2 T35035	probable acyl-[acyl
23	271.5	13.2	338	2 D87182	acyl-[ACPI] desatur
24	256.5	12.4	338	2 H70810	probable desat pro
25	135	6.5	275	2 C87153	acyl-[ACPI] desatur
26	122.5	5.9	2269	2 T28677	rhodry protein -
27	121.5	5.9	275	2 D70896	probable desat pro
28	114.5	5.6	1557	2 T18412	lipid-binding prot
29	108	5.2	616	2 A64341	hypothetical prote

30	105.5	5.1	393	2 C71836	tryptophan synthas
31	105.5	5.1	520	2 P90596	restriction-modifi
32	105.5	5.1	520	2 A99566	restriction-modifi
33	105.5	5.1	684	2 AE2004	hypothetical prote
34	104.5	5.1	524	2 T43050	cyclin E - Caenorh
35	104.5	5.1	570	2 T30156	hypothetical prote
36	103	5.0	244	2 C89811	hypothetical prote
37	102.5	5.0	393	2 F64679	tryptophan synthas
38	102.5	5.0	520	2 S49395	HsdM1 protein - My
39	101.5	4.9	846	2 JC7720	acetyltransferase
40	100.5	4.9	1027	2 T46296	hypothetical prote
41	100.5	4.9	3643	2 T36410	probable polyketid
42	100	4.8	604	2 T19682	hypothetical prote
43	99.5	4.8	517	2 T48283	ankyrin-like prote
44	99.5	4.8	1120	2 JC7765	mitotic spindle as
45	99	4.8	782	2 A82940	hypothetical prote

ALIGNMENTS

RESULT 1

A47245
N:Alternate names: type II acyl-ACP desaturase (EC 1.14.19.2) - coriander
C:Species: Coriandrum sativum (coriander)
C>Date: 21-Jan-1994 #sequence_revise 18-Nov-1994 #text_change 03-Jun-2002
C:Accession: A47245
R:Caenor, E.B.; Shanklin, J.; Ohlrogge, J.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 11184-11188, 1992
A:Title: Expression of a coriander desaturase results in petroselinic acid*production
A:Reference number: A47245; M0ID:93087491; PMID:1454797
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-385 <CAH>
A:Cross-references: GB:M93115; MID:g167388; PIDN:AA63059.1; PID:g167389
A:Note: sequence extracted from NCBI backbone (NCBI:119750, NCBI:P.119751)
C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase

Query Match	75.0%	Score 1545.5;	DB 2;	Length 385;
Best local Similarity	73.1%	Pred. No. 2.6e-105;		
Matches 296;	Conservative 42;	Mismatches 36;	Indels 31;	Gaps 5;
Db	1 MALKNFQCKKHPAAFAKSPLVTRVSP-----RVMASVNSNSVLDNLK 49			
Qy	1 MALKNFQCKKHPAAFAKSPLVTRVSP-----RVMASVNSNSVLDNLK 49			
Db	1 MALKNFQCKKHPAAFAKSPLVTRVSP-----RVMASVNSNSVLDNLK 49			
Qy	50 SPNLAQVTHSMPOKLEIFKSLDDMANNVLIHLKSVKSNQPODYLPDPVSDGFEEOVR 109			
Db	52 AG-----RPEVDLFLNLEGMARDNLIHLKSVKSNQPODYLPDPVSDGFEEOVR 102			
Qy	110 ELERAKKEIPDDYFVVLVGMITEBALPTYMSLNRCDCIDEFGAESAAMAMTRANTA 169			
Db	103 EMERAKKEIPDDYFVVLVGMITEBALPTYMSLNRCDCIDEFGAESAAMAMTRANTA 162			
Qy	170 EENRHGDLNKKYLYLSGRVDMRKTEKTOYLIGSGMDIKSNPPLGFTYVSPORAFPI 229			
Db	163 EENRHGDLNKKYLYLSGRVDMRKTEKTOYLIGSGMDIKSNPPLGFTYVSPORAFPI 222			
Qy	230 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATYTKIVEKLAIEDPPTVYAFADMMRK 289			
Db	223 SHANTAKLAOHYGDKNLAHICGSIASDEKRAHATYTKIVEKLAIEDPPTVYAFADMMRK 282			
Qy	290 KITPAHLMTDGSDELLFKHFTAAQRYXYXSAIDYCDILEFLVDKNVVERLTGSDGR 349			
Db	283 KITPAHLMTDGSDELLFKHFTAAQRYXYXSAIDYCDILEFLVDKNVVERLTGSDGR 342			
Qy	350 KAOYVCELPKIRVVEKVGKREKKKAHPVSPSWIFNRELKI 394			
Db	343 KAOYVCELPKIRVVEKVGKREKKKAHPVSPSWIFNRELKI 385			

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